

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds  
(without alignments)  
65.338 Million cell updates/sec

Title: US-10-056-583A-64  
Perfect score: 70  
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	15	5	Abp52270 HLA-DR2 m
2	65	92.9	15	5	Abp52271 HLA-DR2 m
3	65	92.9	15	5	Abp52272 HLA-DR2 m
4	65	92.9	15	5	Abp52298 HLA-DR2 m
5	65	92.9	17	5	Abp52294 HLA-DR2 m
6	65	92.9	17	5	Abp52296 HLA-DR2 m
7	65	92.9	19	5	Abp52295 HLA-DR2 m
8	64	91.4	15	5	Abp52257 HLA-DR2 m
9	60	85.7	15	5	Abp52290 HLA-DR2 m
10	60	85.7	15	5	Abp52261 HLA-DR2 m
11	60	85.7	15	5	Abp52292 HLA-DR2 m
12	60	85.7	15	5	Abp52269 HLA-DR2 m
13	59	84.3	15	5	Abp52267 HLA-DR2 m
14	59	84.3	15	5	Abp52263 HLA-DR2 m
15	57	81.4	15	5	Abp52301 HLA-DR2 m
16	56	80.0	15	5	Abp52304 HLA-DR2 m
17	56	80.0	17	5	Abp52303 HLA-DR2 m
18	55	78.6	15	5	Abp52291 HLA-DR2 m
19	55	78.6	15	5	Abp52251 HLA-DR2 m
20	55	78.6	15	5	Abp52248 HLA-DR2 m
21	55	78.6	15	5	Abp52268 HLA-DR2 m
22	55	78.6	15	5	Abp52239 HLA-DR2 m
23	54.5	77.9	15	5	Abp52265 HLA-DR2 m
24	54	77.1	15	5	Abp52240 HLA-DR2 m
25	54	77.1	15	5	Abp52241 HLA-DR2 m

26	54	77.1	15	5	Abp52249	HLA-DR2 m
27	53	75.7	15	5	Abp52243	HLA-DR2 m
28	53	75.7	15	5	Abp52258	HLA-DR2 m
29	53	75.7	15	5	Abp52259	HLA-DR2 m
30	53	75.7	15	5	Abp52262	HLA-DR2 m
31	53	75.7	15	5	Abp52260	HLA-DR2 m
32	52	74.3	15	5	Abp52305	HLA-DR2 m
33	52	74.3	17	5	Abp52302	HLA-DR2 m
34	51	72.9	15	5	Abp52255	HLA-DR2 m
35	51	72.9	15	5	Abp52253	HLA-DR2 m
36	51	72.9	15	5	Abp52242	HLA-DR2 m
37	51	72.9	15	5	Abp52297	HLA-DR2 m
38	50	71.4	15	3	AAY58969	Copeptide
39	50	71.4	15	3	AAY82058	HLA class
40	50	71.4	15	4	AA631198	Peptide w
41	50	71.4	15	5	Abp52256	HLA-DR2 m
42	50	71.4	15	5	Abp52289	HLA-DR2 m
43	50	71.4	15	5	Abp52266	HLA-DR2 m
44	50	71.4	15	7	ADJ57542	Cop-1 rel
45	50	71.4	15	8	ADQ59601	Copolymer

## ALIGNMENTS

## RESULT 1

ABP52270  
ID ABP52270 standard; peptide; 15 AA.  
XX ABP52270;  
AC  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

XX Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases



CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 70; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-05; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EAAKYEAYKAAAAA 15  
 Db 1 EAAKYEAYKAAAAA 15  
 |||||  
 RESULT 2  
 ID ABP52271 standard; peptide; 15 AA.  
 AC ABP52271;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 XX WPI; 2002-608439/65.  
 DR  
 XX  
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 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 15 AA;  
 Query Match 92.9%; Score 65; DB 5; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 0.00057; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EAAKYEAYKAAAAA 15  
 Db 1 EAAKYEAYKAAAAA 15  
 |||||  
 RESULT 3  
 ID ABP52272 standard; peptide; 15 AA.  
 XX  
 AC ABP52272;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:66.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 XX WPI; 2002-608439/65.  
 DR  
 XX  
 XX New compositions comprising synthetic peptides in complex with a major  
 XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
 XX encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 CC  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
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 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 92.9%; Score 65; DB 5; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 0.00057; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EAAKYEAYKAAAAA 15



```

Db      1  ||||| 15
        1 EAKYEAYKAAAAA 15

RESULT 4
ABP52298
ID  ABP52298 standard; peptide; 15 AA.
AC      ABP52298;
XX
XX
XX      16-OCT-2002 (first entry)
XX
XX      HLA-DR2 molecule binding peptide SEQ ID NO:2.
XX
XX      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX      immune response; antiinflammatory; neuroprotective; proliferation;
XX      MHC class II protein inhibitor; demyelinating disease; inhibition;
XX      post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX      anti-tumour necrosis factor agent.
XX
XX      Homo sapiens.
XX      OS
XX      Synthetic.
XX
XX      WO200259143-A2.
XX
XX      01-AUG-2002.
XX
XX      24-JAN-2002; 2002WO-US002071.
XX
XX      24-JAN-2001; 2001US-0263569P.
XX
XX      (HARD ) HARVARD COLLEGE.
XX
XX      Strominger JL, Fridkis-Hareli M;
XX
XX      WPI; 2002-608439/65.
XX
XX      New compositions comprising synthetic peptides in complex with a major
XX      histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX      demyelinating disease, e.g. multiple sclerosis, or post-viral
XX      encephalomyelitis.
XX
XX      Claim 28; Page 39; 54pp; English.
XX
XX      The present invention describes compositions (I) comprising a peptide
XX      with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX      residues. The complex of the peptide with a major histocompatibility
XX      complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX      immune response. (I) has antiinflammatory and neuroprotective activities,
XX      and can be used as a MHC class II protein inhibitor. The compositions
XX      comprising the peptides are useful for treating demyelinating diseases
XX      such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
XX      demyelinating condition, and a side effect of administering an anti-
XX      tumour necrosis factor agents. The peptide further inhibits proliferation
XX      of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
XX      ABP52305 represent peptides used in the exemplification of the present
XX      invention
XX
XX      Sequence 15 AA;
XX
XX      Query Match      92.9%; Score 65; DB 5; Length 15;
XX      Best Local Similarity 93.3%; Pred. No. 0.00057;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EAKYEAYKAAAAA 15
DB      1  ||||| 15
        1 EAKYEAYKAAAAA 15

RESULT 5
ABP52299
ID  ABP52299 standard; peptide; 17 AA.
AC      ABP52299;
XX
XX
XX      16-OCT-2002 (first entry)
XX
XX      HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
XX      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX      immune response; antiinflammatory; neuroprotective; proliferation;
XX      MHC class II protein inhibitor; demyelinating disease; inhibition;
XX      post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX      anti-tumour necrosis factor agent.
XX
XX      Homo sapiens.
XX      OS
XX      Synthetic.
XX
XX      WO200259143-A2.
XX
XX      01-AUG-2002.
XX
XX      24-JAN-2002; 2002WO-US002071.
XX
XX      24-JAN-2001; 2001US-0263569P.
XX
XX      (HARD ) HARVARD COLLEGE.
XX
XX      Strominger JL, Fridkis-Hareli M;
XX
XX      WPI; 2002-608439/65.
XX
XX      New compositions comprising synthetic peptides in complex with a major
XX      histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX      demyelinating disease, e.g. multiple sclerosis, or post-viral
XX      encephalomyelitis.
XX
XX      Claim 28; Page 39; 54pp; English.
XX
XX      The present invention describes compositions (I) comprising a peptide
XX      with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX      residues. The complex of the peptide with a major histocompatibility
XX      complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX      immune response. (I) has antiinflammatory and neuroprotective activities,
XX      and can be used as a MHC class II protein inhibitor. The compositions
XX      comprising the peptides are useful for treating demyelinating diseases
XX      such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
XX      demyelinating condition, and a side effect of administering an anti-
XX      tumour necrosis factor agents. The peptide further inhibits proliferation
XX      of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
XX      ABP52305 represent peptides used in the exemplification of the present
XX      invention
XX
XX      Sequence 17 AA;
XX
XX      Query Match      92.9%; Score 65; DB 5; Length 17;
XX      Best Local Similarity 93.3%; Pred. No. 0.00065;
XX      Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EAKYEAYKAAAAA 15
DB      3  ||||| 17
        3 EAKYEAYKAAAAA 17

RESULT 6
ABP52296
ID  ABP52296 standard; peptide; 17 AA.
AC      ABP52296;
XX
XX
XX      16-OCT-2002 (first entry)
XX
XX      HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
XX

```



KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200259143-A2.  
 PN 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX 24-JAN-2001; 2001US-0263569P.  
 XX (HARD ) HARVARD COLLEGE.  
 PA Strominger JL, Fridekis-Hareli M;  
 PI WPI; 2002-608439/65.  
 XX  
 XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
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 XX Claim 28; Page 39; 54pp; English.  
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 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 92.9%; Score 65; DB 5; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 0.00065;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EAAKYEAYKAAAAA 15  
 Db 1 EKAKYEAYKAAAAA 15  
 RESULT 7  
 ABP52295  
 ID ABP52295 standard; peptide; 19 AA.  
 XX  
 AC ABP52295;  
 XX  
 XX 16-OCT-2002 (first entry)  
 DT  
 XX HLA-DR2 molecule binding peptide SEQ ID NO:89.  
 DE  
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX WO200259143-A2.  
 XX 01-AUG-2002.  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX 24-JAN-2001; 2001US-0263569P.  
 XX (HARD ) HARVARD COLLEGE.  
 PA Strominger JL, Fridekis-Hareli M;  
 PI WPI; 2002-608439/65.  
 XX  
 XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
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 XX The present invention describes compositions (I) comprising a peptide  
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 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
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 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 19 AA;  
 SQ  
 Query Match 92.9%; Score 65; DB 5; Length 19;  
 Best Local Similarity 93.3%; Pred. No. 0.00073;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EAAKYEAYKAAAAA 15  
 Db 3 EKAKYEAYKAAAAA 17  
 RESULT 8  
 ABP52257  
 ID ABP52257 standard; peptide; 15 AA.  
 XX  
 AC ABP52257;  
 XX  
 XX 16-OCT-2002 (first entry)  
 DT  
 XX HLA-DR2 molecule binding peptide SEQ ID NO:51.  
 DE  
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200259143-A2.  
 XX 01-AUG-2002.  
 XX



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PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
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XX
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CC demyelinating condition, and a side effect of administering an anti-
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CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 91.4%; Score 64; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00083;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
DB ||||| |||||
1 EAAKYEAYKAAAAA 15

RESULT 9
ABP52290
ID ABP52290 standard; peptide; 15 AA.
XX
XX
AC ABP52290;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
PF
XX
XX 24-JAN-2001; 2001US-0263569P.
PR
XX
XX (HARD ) HARVARD COLLEGE.
PA
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PI
WPI; 2002-608439/65.
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CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 85.7%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
DB ||||| |||||
1 EAPKYEAYKAAAAA 15

RESULT 10
ABP52261
ID ABP52261 standard; peptide; 15 AA.
XX
XX
AC ABP52261;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:55.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
PF
XX
XX 24-JAN-2001; 2001US-0263569P.
PR
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

```



xx Example 1; Page 33; 54pp; English.

xx The present invention describes compositions (I) comprising a peptide

xx with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

xx residues. The complex of the peptide with a major histocompatibility

xx complex (MHC) class II HLA-DR2 protein is involved in modulating an

xx immune response. (I) has antiinflammatory and neuroprotective activities,

xx and can be used as a MHC class II protein inhibitor. The compositions

xx comprising the peptides are useful for treating demyelinating diseases

xx such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

xx demyelinating condition, and a side effect of administering an anti-

xx tumour necrosis factor agents. The peptide further inhibits proliferation

xx of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

xx ABP52305 represent peptides used in the exemplification of the present

xx invention

xx Sequence 15 AA;

xx

xx Query Match 85.7%; Score 60; DB 5; Length 15;

xx Best Local Similarity 86.7%; Pred. No. 0.0037;

xx Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAAA 15

Db 1 EAAEYAAAYKAAAAAA 15

|||||

RESULT 11

ABP52292

ID ABP52292 standard; peptide; 15 AA.

AC ABP52292;

XX

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:86.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

PN 01-AUG-2002.

XX

XX 24-JAN-2002; 2002WO-US002071.

PF

XX 24-JAN-2001; 2001US-0263569P.

PR (HARD ) HARVARD COLLEGE.

XX

XX Strominger JL, Fridkis-Hareli M;

PI WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

xx histocompatibility complex class II HLA-DR2 protein, useful for treating a

xx demyelinating disease, e.g. multiple sclerosis, or post-viral

xx encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

xx

xx The present invention describes compositions (I) comprising a peptide

xx with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

xx residues. The complex of the peptide with a major histocompatibility

xx complex (MHC) class II HLA-DR2 protein is involved in modulating an

xx immune response. (I) has antiinflammatory and neuroprotective activities,

xx and can be used as a MHC class II protein inhibitor. The compositions

xx comprising the peptides are useful for treating demyelinating diseases

xx such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

xx demyelinating condition, and a side effect of administering an anti-

xx tumour necrosis factor agents. The peptide further inhibits proliferation

xx of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

xx ABP52305 represent peptides used in the exemplification of the present

xx invention

xx Sequence 15 AA;

xx

xx Query Match 85.7%; Score 60; DB 5; Length 15;

xx Best Local Similarity 86.7%; Pred. No. 0.0037;

xx Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAAA 15

Db 1 EAAEYAAAYKAAAAAA 15

|||||

RESULT 12

ABP52269

ID ABP52269 standard; peptide; 15 AA.

AC ABP52269;

XX

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:63.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

PN 01-AUG-2002.

XX

XX 24-JAN-2002; 2002WO-US002071.

PF

XX 24-JAN-2001; 2001US-0263569P.

PR (HARD ) HARVARD COLLEGE.

XX

XX Strominger JL, Fridkis-Hareli M;

PI WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

xx histocompatibility complex class II HLA-DR2 protein, useful for treating a

xx demyelinating disease, e.g. multiple sclerosis, or post-viral

xx encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

xx

xx The present invention describes compositions (I) comprising a peptide

xx with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

xx residues. The complex of the peptide with a major histocompatibility

xx complex (MHC) class II HLA-DR2 protein is involved in modulating an

xx immune response. (I) has antiinflammatory and neuroprotective activities,

xx and can be used as a MHC class II protein inhibitor. The compositions

xx comprising the peptides are useful for treating demyelinating diseases

xx such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

xx demyelinating condition, and a side effect of administering an anti-

xx tumour necrosis factor agents. The peptide further inhibits proliferation

xx of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

xx ABP52305 represent peptides used in the exemplification of the present

xx invention

xx Sequence 15 AA;

xx

xx Query Match 85.7%; Score 60; DB 5; Length 15;

xx Best Local Similarity 86.7%; Pred. No. 0.0037;

xx Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAAA 15

Db 1 EAPKYEAYKAAAPA 15

|||||

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

XX

XX Query Match 85.7%; Score 60; DB 5; Length 15;

XX Best Local Similarity 86.7%; Pred. No. 0.0037;

XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAAA 15

Db 1 EAPKYEAYKAAAPA 15

|||||

RESULT 12

ABP52269

ID ABP52269 standard; peptide; 15 AA.

AC ABP52269;

XX

XX 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:63.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

PN 01-AUG-2002.

XX

XX 24-JAN-2002; 2002WO-US002071.

PF

XX 24-JAN-2001; 2001US-0263569P.

PR (HARD ) HARVARD COLLEGE.

XX

XX Strominger JL, Fridkis-Hareli M;

PI WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

xx histocompatibility complex class II HLA-DR2 protein, useful for treating a

xx demyelinating disease, e.g. multiple sclerosis, or post-viral

xx encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

xx

xx The present invention describes compositions (I) comprising a peptide

xx with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

xx residues. The complex of the peptide with a major histocompatibility

xx complex (MHC) class II HLA-DR2 protein is involved in modulating an

xx immune response. (I) has antiinflammatory and neuroprotective activities,

xx and can be used as a MHC class II protein inhibitor. The compositions

xx comprising the peptides are useful for treating demyelinating diseases

xx such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

xx demyelinating condition, and a side effect of administering an anti-

xx tumour necrosis factor agents. The peptide further inhibits proliferation

xx of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

xx ABP52305 represent peptides used in the exemplification of the present

xx invention

xx Sequence 15 AA;

xx

xx Query Match 85.7%; Score 60; DB 5; Length 15;

xx Best Local Similarity 86.7%; Pred. No. 0.0037;

xx Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAAA 15

Db 1 EAPKYEAYKAAAPA 15

|||||



CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;

Query Match 85.7%; Score 60; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.0037; 1; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
 |||:|||||||  
 Db 1 EAAKYEAYKAAAAA 15

RESULT 13  
 ABP52267  
 ID ABP52267 standard; peptide; 15 AA.  
 XX  
 AC ABP52267;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:61.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 DR WPI; 2002-608439/65.  
 XX  
 PT New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Example 1; Page 33; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agent. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;

Query Match 84.3%; Score 59; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.0055;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
 |||:|||||||  
 Db 1 EAAKYEAYKAAAAA 15

RESULT 14  
 ABP52263  
 ID ABP52263 standard; peptide; 15 AA.  
 XX  
 AC ABP52263;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:57.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 DR WPI; 2002-608439/65.  
 XX  
 PT New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Example 1; Page 33; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agent. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;

Query Match 84.3%; Score 59; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.0055;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
 |||:|||||||  
 Db 1 EAAKYEAYKAAAAA 15



**RESULT 15**

ABP52301  
ID ABP52301 standard; peptide; 15 AA.

XX AC ABP52301;  
XX AC ABP52301;

DT 16-OCT-2002 (first entry)

XX XX  
XX XX  
XX XX  
KW KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW KW anti-tumour necrosis factor agent.  
XX XX  
XX OS Homo sapiens.  
OS OS Synthetic.  
XX XX  
XX PN W0200259143-A2.  
XX PD 01-AUG-2002.  
XX PP 24-JAN-2002; 2002WO-US002071.  
XX PF 24-JAN-2001; 2001US-0263569P.  
XX PR (HARD ) HARVARD COLLEGE.  
XX PA Strominger JL, Fridkis-Hareli M;  
XX PI WPI; 2002-608439/65.  
XX DR  
XX XX  
XX PT New compositions comprising synthetic peptides in complex with a major  
XX PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
XX PT encephalomyelitis.  
XX PS Claim 28; Page 39; 54pp; English.  
XX CC The present invention describes compositions (I) comprising a peptide  
XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX CC residues. The complex of the peptide with a major histocompatibility  
XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
XX CC immune response. (I) has antiinflammatory and neuroprotective activities,  
XX CC and can be used as a MHC class II protein inhibitor. The compositions  
XX CC comprising the peptides are useful for treating demyelinating diseases  
XX CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
XX CC demyelinating condition, and a side effect of administering an anti-  
XX CC tumour necrosis factor agents. The peptide further inhibits proliferation  
XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
XX CC ABP52305 represent peptides used in the exemplification of the present  
XX CC invention  
XX XX  
SQ Sequence 15 AA;

Query Match 81.4%; Score 57; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.012;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0

QY 1 EAAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
DB 1 EKAKFEAFKAAAAA 15

Search completed: March 31, 2005, 02:35:27  
Job time : 89.7903 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds  
(without alignments)  
48.718 Million cell updates/sec

Title: US-10-056-583A-64  
Perfect score: 70  
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 slides

Database : Issued Patents AA:\*

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2: /cgn2_6/pctodata/1/iaa/5B_COMB.pcp.*
3: /cgn2_6/pctodata/1/iaa/6A_COMB.pcp.*
4: /cgn2_6/pctodata/1/iaa/6B_COMB.pcp.*
5: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pcp.*
6: /cgn2_6/pctodata/1/iaa/backfiles.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			Description		
	Score	Match	Length	ID	DB	Description
1	42	60.0	13	5	PCT-US95-04121-38	Sequence 38, Appl
2	40	57.1	13	5	PCT-US94-10257A-33	Sequence 33, Appl
3	40	57.1	391	1	US-09-902-540-11110	Sequence 11110, A
4	40	57.1	466	1	US-09-489-039A-13950	Sequence 13950, A
5	39.5	56.4	21	1	US-07-988-754-4	Sequence 4, Appl
6	39.5	56.4	33	1	US-07-988-754-12	Sequence 12, Appl
7	39	55.7	186	4	US-09-902-540-11242	Sequence 11242, A
8	39	55.7	596	2	US-08-836-620A-16	Sequence 16, Appl
9	39	55.7	601	4	US-09-252-991A-18124	Sequence 18124, A
10	39	55.7	731	4	US-09-252-991A-18769	Sequence 18769, A
11	38.5	55.0	86	4	US-09-405-743A-6	Sequence 6, Appl
12	38.5	55.0	86	4	US-09-816-989A-6	Sequence 6, Appl
13	38	54.3	64	4	US-09-248-796A-26627	Sequence 26627, A
14	38	54.3	407	4	US-09-252-991A-29581	Sequence 29581, A
15	38	54.3	534	4	US-09-252-991A-32086	Sequence 32086, A
16	37	52.9	20	1	US-08-440-861-23	Sequence 23, Appl
17	37	52.9	25	6	5169933-42	Patent No. 5169933
18	37	52.9	25	6	5169933-42	Patent No. 5169933
19	37	52.9	109	4	US-09-405-743A-7	Sequence 7, Appl
20	37	52.9	109	4	US-09-816-989A-7	Sequence 7, Appl
21	37	52.9	301	1	US-08-440-861-2	Sequence 2, Appl
22	37	52.9	301	1	US-08-433-854-2	Sequence 2, Appl
23	37	52.9	301	1	US-08-174-745A-2	Sequence 2, Appl
24	37	52.9	301	2	US-08-195-947-2	Sequence 2, Appl
25	37	52.9	301	2	US-08-433-885-2	Sequence 2, Appl
26	37	52.9	301	2	US-08-433-908B-2	Sequence 2, Appl
27	37	52.9	301	3	US-08-410-614-2	Sequence 2, Appl

28	37	52.9	400	4	US-09-270-767-46186	Sequence 46186, A
29	37	52.9	426	3	US-08-961-083-48	Sequence 48, Appl
30	37	52.9	426	4	US-08-961-083-48	Sequence 48, Appl
31	37	52.9	427	3	US-09-536-784-48	Sequence 2, Appl
32	37	52.9	427	3	US-09-136-857-2	Sequence 2, Appl
33	37	52.9	427	4	US-09-583-110-3940	Sequence 3940, Ap
34	37	52.9	435	4	US-09-107-433-4256	Sequence 4256, Ap
35	37	52.9	435	4	US-09-543-681A-5116	Sequence 5116, Ap
36	37	52.9	497	1	US-08-295-670-6	Sequence 6, Appl
37	37	52.9	497	1	US-08-633-485-6	Sequence 6, Appl
38	37	52.9	510	3	US-08-508-761B-4	Sequence 4, Appl
39	37	52.9	802	4	US-09-489-0319A-11230	Sequence 11230, A
40	37	52.9	1001	4	US-09-248-796A-1858	Sequence 1858, A
41	36.5	52.1	741	4	US-09-949-016-11523	Sequence 11523, A
42	36.5	52.1	741	4	US-09-949-016-11524	Sequence 11524, A
43	36	51.4	13	5	PCT-US95-04121-60	Sequence 60, Appl
44	36	51.4	37	3	US-09-117-121-42	Sequence 42, Appl
45	36	51.4	45	4	US-09-405-743A-2	Sequence 2, Appl
46	36	51.4	45	4	US-09-816-989A-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
 PCI-US95-04121-38  
 Sequence 38, Application PC/TUS9504121  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: Haptenated Peptides and Uses Thereof  
 NUMBER OF SEQUENCES: 62  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04121  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/222,206  
 FILING DATE: April 1, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Vanstone, Darlene A.  
 REGISTRATION NUMBER: 35,279  
 REFERENCE/DOCKET NUMBER: 079.2PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 466-6000  
 TELEFAX: (617) 466-6010  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 PCT-US95-04121-38

Query Match 60.0%; Score 42; DB 5; Length 13;  
Best Local Similarity 76.9%; Pred. No. 0.82;  
Matches 10: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

Qy 3 AKYEAYKAAAAA 15  
| | : | | | | |  
Db 1 AAYKAAKAAAAA 13

RESULT 2  
PCT-US94-10257A-33  
; Sequence 33, Application PC/TUS9410257A  
; GENERAL INFORMATION:  
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION



APPLICANT: BRIGITTE DEVAUX  
APPLICANT: JONATHAN B. ROTHBEARD  
APPLICANT: DAWN SMILEX  
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE  
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS  
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10257A  
FILING DATE: 1 SEPTEMBER 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,824  
FILING DATE: 03-SEP-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ANNE I CRAIG  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 071.1 PCT  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-10257A-33

Query Match 57.1%; Score 40; DB 5; Length 13;  
Best Local Similarity 76.9%; Pred. No. 1.7;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 15  
| | | | |  
Db 1 AAYAAKAAAAA 13

RESULT 3  
US-09-902-540-11110  
; Sequence 1110, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1110  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-11110

Query Match 57.1%; Score 40; DB 4; Length 391;  
Best Local Similarity 53.3%; Pred. No. 59;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAAKYAYKAAAAA 15  
| | | | |  
Db 81 KAEAYRAYKASGSA 95

RESULT 4  
US-09-489-039A-13950  
; Sequence 13950, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13950  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13950

Query Match 57.1%; Score 40; DB 4; Length 466;  
Best Local Similarity 76.9%; Pred. No. 71;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 15  
| | | | |  
Db 153 ASLEAQKAAAAA 165

RESULT 5  
US-07-988-754-4  
; Sequence 4, Application US/07988754  
; Patent No. 5374431  
; GENERAL INFORMATION:  
; APPLICANT: Pang, Roy H.L.  
; APPLICANT: Cohen, Charles M.  
; APPLICANT: Keck, Peter C.  
; TITLE OF INVENTION: Synthetic Bioadhesive  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Creative Biomolecules  
; STREET: 35 South Street  
; CITY: Hopkinton  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 01748  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,754  
; FILING DATE: 19921210  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,323  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G.  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: CRP-046  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 435-9001



TELEFAX: (508) 435-6951  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-07-988-754-4

Query Match 56.4%; Score 39.5; DB 1; Length 21;  
Best Local Similarity 68.8%; Pred. No. 3.4;  
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 2 AAKYE---AYKAAAA 14  
||||: ||| ||||  
DB 2 AAKYKAAAYKYAAAA 17

## RESULT 6

US-07-988-754-12  
; Sequence 12, Application US/07988754  
; Patent No. 5374431  
; GENERAL INFORMATION:

; APPLICANT: Pang, Roy H.L.  
; APPLICANT: Cohen, Charles M.  
; APPLICANT: Keck, Peter C.  
; TITLE OF INVENTION: Synthetic Bioadhesive  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Creative Biomolecules  
; STREET: 35 South Street  
; CITY: Hopkinton  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 01748

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,754  
; FILING DATE: 19921210  
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/627,323  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G.  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: CRP-046  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 435-9001  
; TELEFAX: (508) 435-6951  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-988-754-12

Query Match 56.4%; Score 39.5; DB 1; Length 33;  
Best Local Similarity 68.8%; Pred. No. 5.5;  
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 2 AAKYE---AYKAAAA 14  
||||: ||| ||||  
DB 4 AAKYKAAAYKYAAAA 19

## RESULT 7

US-09-902-540-11242  
; Sequence 11242, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 11242  
; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-11242

Query Match 55.7%; Score 39; DB 4; Length 186;  
Best Local Similarity 61.5%; Pred. No. 40;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAA 14  
:|: |||||  
DB 48 SASYQYKAAADA 60

## RESULT 8

US-08-836-620A-16  
; Sequence 16, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,620A  
; FILING DATE:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP96/03933  
; FILING DATE:  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 596 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORGANISM: Rattus rattus  
US-08-836-620A-16

Query Match 55.7%; Score 39; DB 2; Length 596;



Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
DB 56 EGAAYEFNAAAAA 70

RESULT 9  
US-09-252-991A-21824  
; Sequence 21824, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21824  
; LENGTH: 601  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (601)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-21824

Query Match 55.7%; Score 39; DB 4; Length 601;  
Best Local Similarity 58.3%; Pred. No. 1.3e+02;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 14  
DB 570 ARYEAYRSAIVA 581

RESULT 10  
US-09-252-991A-18769  
; Sequence 18769, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18769  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18769

Query Match 55.7%; Score 39; DB 4; Length 731;  
Best Local Similarity 72.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15  
DB 179 YEAYEACARA 189

RESULT 11  
US-09-405-743A-6  
; Sequence 6, Application US/09405743A  
; Patent No. 6514938  
; GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co., Ltd.  
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS  
; FILE REFERENCE: 60807-A  
; CURRENT APPLICATION NUMBER: US/09/405,743A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
US-09-405-743A-6

Query Match 55.0%; Score 38.5; DB 4; Length 86;  
Best Local Similarity 73.3%; Pred. No. 22;  
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EAAKYEAYKAAAAA 15  
DB 64 EAAK-KAYKAEAAKA 77

RESULT 12  
US-09-816-989A-6  
; Sequence 6, Application US/09816989A  
; Patent No. 6800287  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; APPLICANT: Lis, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS  
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE  
; FILE REFERENCE: 2609/60807-A-ECT-US  
; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101,693  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-6

Query Match 55.0%; Score 38.5; DB 4; Length 86;  
Best Local Similarity 73.3%; Pred. No. 22;  
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EAAKYEAYKAAAAA 15  
DB 64 EAAK-KAYKAEAAKA 77

RESULT 13  
US-09-248-796A-26627  
; Sequence 26627, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS



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, TITLE OF INVENTION: AEROGELINOSA FOR DIAGNOSIS
, FILE REFERENCE: 107196.136
, CURRENT APPLICATION NUMBER: US/09/252,991A
, CURRENT FILING DATE: 1999-02-18
, PRIOR APPLICATION NUMBER: US 60/074,788
, PRIOR FILING DATE: 1998-02-18
, PRIOR APPLICATION NUMBER: US 60/094,190
, PRIOR FILING DATE: 1998-07-27
, NUMBER OF SEQ ID NOS: 33142
, SEQ ID NO 32086
, LENGTH: 534

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds  
(without alignments)  
74.648 Million cell updates/sec

Title: US-10-056-583A-64  
Perfect score: 70  
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	65	92.9	15	14	US-10-056-583-65
3	65	92.9	15	14	US-10-056-583-66
4	65	92.9	17	14	US-10-056-583-88
5	65	92.9	17	14	US-10-056-583-90
6	65	92.9	19	14	US-10-056-583-89
7	64	91.4	15	14	US-10-056-583-51
8	60	85.7	15	14	US-10-056-583-55
9	60	85.7	15	14	US-10-056-583-63
10	60	85.7	15	14	US-10-056-583-84
11	60	85.7	15	14	US-10-056-583-86
12	59	84.3	15	14	US-10-056-583-57
13	59	84.3	15	14	US-10-056-583-61

14	57	81.4	15	14	US-10-056-583-95	Sequence 95, Appl
15	56	80.0	15	14	US-10-056-583-92	Sequence 92, Appl
16	56	80.0	15	14	US-10-056-583-98	Sequence 98, Appl
17	56	80.0	17	14	US-10-056-583-97	Sequence 97, Appl
18	55	78.6	15	14	US-10-056-583-33	Sequence 33, Appl
19	55	78.6	15	14	US-10-056-583-42	Sequence 42, Appl
20	55	78.6	15	14	US-10-056-583-45	Sequence 45, Appl
21	55	78.6	15	14	US-10-056-583-62	Sequence 62, Appl
22	55	78.6	15	14	US-10-056-583-85	Sequence 85, Appl
23	54.5	77.9	15	14	US-10-056-583-59	Sequence 59, Appl
24	54	77.1	15	14	US-10-056-583-34	Sequence 34, Appl
25	54	77.1	15	14	US-10-056-583-35	Sequence 35, Appl
26	54	77.1	15	14	US-10-056-583-43	Sequence 43, Appl
27	53	75.7	15	14	US-10-056-583-37	Sequence 37, Appl
28	53	75.7	15	14	US-10-056-583-52	Sequence 52, Appl
29	53	75.7	15	14	US-10-056-583-53	Sequence 53, Appl
30	53	75.7	15	14	US-10-056-583-54	Sequence 54, Appl
31	53	75.7	15	14	US-10-056-583-56	Sequence 56, Appl
32	52	74.3	15	14	US-10-056-583-99	Sequence 99, Appl
33	52	74.3	17	14	US-10-056-583-96	Sequence 96, Appl
34	51	72.9	15	14	US-10-056-583-36	Sequence 36, Appl
35	51	72.9	15	14	US-10-056-583-47	Sequence 47, Appl
36	51	72.9	15	14	US-10-056-583-49	Sequence 49, Appl
37	51	72.9	15	14	US-10-056-583-91	Sequence 91, Appl
38	50	71.4	15	9	US-09-765-301-24	Sequence 24, Appl
39	50	71.4	15	10	US-09-765-644A-24	Sequence 24, Appl
40	50	71.4	15	14	US-10-056-583-50	Sequence 50, Appl
41	50	71.4	15	14	US-10-056-583-60	Sequence 60, Appl
42	50	71.4	15	14	US-10-056-583-83	Sequence 83, Appl
43	50	71.4	15	15	US-10-438-538-28	Sequence 28, Appl
44	49	70.0	15	14	US-10-056-583-26	Sequence 26, Appl
45	49	70.0	15	14	US-10-056-583-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-10-056-583-64  
; Sequence 64, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-64

Query Match 100.0%; Score 70; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EAAKYEAYKAAAAA 15

RESULT 2  
US-10-056-583-65



```

; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65

```

```

Query Match          92.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EAAKYEAYKAAAAAA 15
   | | | | | | | | | |
Db 1 EAKYEAYKAAAAAA 15

```

```

RESULT 3
US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

```

```

Query Match          92.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EAAKYEAYKAAAAAA 15
   | | | | | | | | | |
Db 1 EAKYEAYKAAAAAA 15

```

```

RESULT 4
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.

```

```

; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

```

```

Query Match          92.9%; Score 65; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EAAKYEAYKAAAAAA 15
   | | | | | | | | | |
Db 3 EAKYEAYKAAAAAA 17

```

```

RESULT 5
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

```

```

Query Match          92.9%; Score 65; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EAAKYEAYKAAAAAA 15
   | | | | | | | | | |
Db 1 EAKYEAYKAAAAAA 15

```

```

RESULT 6
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583

```



; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569.  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-89

Query Match 92.9%; Score 65; DB 14; Length 19;  
Best Local Similarity 93.3%; Pred. No. 0.00074;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
DB 3 EAAKYEAYKAAAAA 17

RESULT 7  
US-10-056-583-51  
; Sequence 51, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 91.4%; Score 64; DB 14; Length 15;  
Best Local Similarity 93.3%; Pred. No. 0.00084;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
DB 1 EAAKYEAYKAAAAA 15

RESULT 8  
US-10-056-583-55  
; Sequence 55, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 55  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-55

Query Match 85.7%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0037;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
DB 1 EAAKYEAYKAAAAA 15

RESULT 9  
US-10-056-583-63  
; Sequence 63, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-63

Query Match 85.7%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0037;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
DB 1 EAAKYEAYKAAAAA 15

RESULT 10  
US-10-056-583-84  
; Sequence 84, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:



us-10-056-583a-64.rapb

Thu Mar 31 14:05:32 2005

OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-84

Query Match 85.7%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0037; Mismatches 2; Indels 0; Gaps 0;  
Matches 13; Conservative 0;

Qy 1 EAAKYEAYKAAAAA 15  
Db 1 EAPKYEAYKAAAPA 15

RESULT 11  
US-10-056-583-86  
; Sequence 86, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-86

Query Match 85.7%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0037; Mismatches 2; Indels 0; Gaps 0;  
Matches 13; Conservative 0;

Qy 1 EAAKYEAYKAAAAA 15  
Db 1 EAPKYEAYKAAAPA 15

RESULT 12  
US-10-056-583-57  
; Sequence 57, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-57

Query Match 84.3%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0054;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAAAA 15  
Db 1 EAAKYEAYKAAAAA 15

RESULT 13  
US-10-056-583-61  
; Sequence 61, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-61

Query Match 84.3%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0054; Mismatches 2; Indels 0; Gaps 0;  
Matches 13; Conservative 0;

Qy 1 EAAKYEAYKAAAAA 15  
Db 1 EAAKYEAYKAAAAA 15

RESULT 14  
US-10-056-583-95  
; Sequence 95, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-95

Query Match 81.4%; Score 57; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.011; Mismatches 2; Indels 1; Gaps 0;  
Matches 12; Conservative 0;

Qy 1 EAAKYEAYKAAAAA 15  
Db 1 EAKAFKFAKAAAAA 15



RESULT 15  
US-10-056-583-92  
; Sequence 92, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-92

Query Match 80.0%; Score 56; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.016;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAAAA 15  
| | | | | | | | | |  
Db 1 EKAKEEAYKAAAAA 15

Search completed: March 31, 2005, 02:48:48  
Job time : 67.5323 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds  
(without alignments)  
80.614 Million cell updates/sec

Title: US-10-056-583A-64

Perfect score: 70

Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	60.0	188	2 IS0145	homeotic protein Hox M - chicken
2	42	60.0	254	2 H86355	probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana
3	42	60.0	289	2 A43562	homeotic protein Hox M - chicken
4	42	60.0	527	2 E9351	phosphoglycerate dehydrogenase
5	41	58.6	124	2 E84764	hypothetical protein
6	41	58.6	1857	1 S01787	fatty-acid synthase
7	41	58.6	2129	2 T27431	hypothetical protein
8	40	57.1	251	2 C70521	1-acylglycerol-3-phosphate
9	40	57.1	354	1 GNVSR	genome polyprotein
10	40	57.1	788	2 F97547	probable oxidoreductase
11	40	57.1	788	2 AC2767	formate dehydrogenase
12	40	57.1	806	2 T13690	hypothetical protein
13	40	57.1	1151	2 T18535	high molecular mass
14	39	55.7	101	2 G75512	conserved hypothetical
15	39	55.7	170	2 E81312	probable lipoprotein
16	39	55.7	250	2 T51971	proteasome endopeptidase
17	39	55.7	519	2 S39893	rnfC protein - Rho
18	39	55.7	553	2 D83640	hypothetical protein
19	39	55.7	599	1 QRMSE	estrogen receptor
20	39	55.7	600	1 QRTE	estrogen receptor
21	39	55.7	698	2 T32594	hypothetical protein
22	39	55.7	728	2 H82965	DNA helicase II PA
23	38	54.3	108	2 F97521	VCO33 protein homo
24	38	54.3	108	2 A42740	conserved hypothetical
25	38	54.3	261	2 T51222	hypothetical protein
26	38	54.3	331	1 D8ECG3	glyceroldehyde-3-phosphate
27	38	54.3	331	2 AG0711	glyceroldehyde-3-phosphate
28	38	54.3	331	2 D85788	glyceroldehyde-3-phosphate
29	38	54.3	331	2 H90939	glyceroldehyde-3-phosphate

conserved hypothetical  
TolA protein PA097  
probable fatty-acyl  
tetrahydrofolylpol  
folylpolylglutamate  
hypothetical prote  
ATPase, AAA family  
H+-transporting tw  
efflux system prot  
related to protein  
probable fatty-acy  
fatty acid synthas  
ribosomal protein  
transcription regu  
T-cell receptor ga  
exoskeletal protei

#### ALIGNMENTS

##### RESULT 1

IS0145

homeotic protein Hox M - chicken

N:Alternate names: CHOX M

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2004

C:Accession: IS0145; S14512

R:Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.

Leukemia 5, 357-360, 1991

A:Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vir

A:Reference number: IS0145; MUID:91238215; PMID:1674560

A:Accession: IS0145

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-188 <CRO>

A:Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; FIDN:CAA40445.1; PID:g62700

C:Genetics:

A:Gene: CHOX M

C:Superfamily: homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:96-152/Domain: homeobox homology <Hox>

Query Match 60.0%; Score 42; DB 2; Length 188;  
Best Local Similarity 81.8%; Pred. No. 9.8;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15

Db 10 YSKYKAAAAA 20

##### RESULT 2

H86355

probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: H86355

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maifi, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: H86141; MUID:21016719; PMID:11130712

A:Accession: H86355

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-254 <STO>



A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:GN  
C;Genetics:  
C;Superfamily: 14-3-3 protein

Query Match 60.0%; Score 42; DB 2; Length 254;  
Best Local Similarity 70.6%; Pred. No. 13;  
Matches 12; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EAA--KYEAYKAAAAA 15  
||| ||||| |||||  
Db 144 EAADQSLEAYKAAVAAA 160

RESULT 3  
A43562  
homeotic protein Hox D8 - mouse  
N;Alternate names: homeotic protein Hox 4.3  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 09-Jul-2004  
C;Accession: A43562  
R;Rizpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou  
Development 110, 733-745, 1990  
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobd  
A;Reference number: A43562; MUID:91209232; PMID:1982431  
A;Accession: A43562  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-289 <IZP>  
A;Cross-references: UNIPROT:P23463  
C;Superfamily: homeotic protein Hox A7; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;196-252/Domain: homeobox homology <HOX>

Query Match 60.0%; Score 42; DB 2; Length 289;  
Best Local Similarity 81.8%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15  
| |||||  
Db 10 YSKYKAAAAA 20

RESULT 4  
E69351  
phosphoglycerate dehydrogenase (serA) homolog - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69351  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A63250; MUID:98049343; PMID:9389475  
A;Accession: E69351  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-527 <KLE>  
A;Cross-references: UNIPROT:O29445; GB:AE001048; GB:AE000782; NID:g2689371; PIDN:AAB9042  
C;Superfamily: Bacillus phosphoglycerate dehydrogenase

Query Match 60.0%; Score 42; DB 2; Length 527;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
||| ||||| |||||  
Db 236 EAALYEAIKAGKVA 250

RESULT 5  
E84764  
hypothetical protein At2g35090 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E84764  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: E84764  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-124 <STO>  
A;Cross-references: UNIPROT:O82182; GB:AE002093; NID:g3668094; PIDN:AAAC61826.1; GSPDB:GN  
C;Genetics:  
A;Gene: At2g35090  
A;Map position: 2

Query Match 58.6%; Score 41; DB 2; Length 124;  
Best Local Similarity 60.0%; Pred. No. 9.7;  
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
||| ||||| |||||  
Db 99 EAVKYAAYTLVAVAA 113

RESULT 6  
S01787  
fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum  
N;Alternate names: fatty acid synthetase  
C;Species: Penicillium griseofulvum  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S01787  
R;Wiesner, P.; Beck, J.; Beck, K.F.; Ripka, S.; Mueller, G.; Luecke, S.; Schweizer, E.  
Eur. J. Biochem 177, 69-79, 1988  
A;Title: Isolation and sequence analysis of the fatty acid synthetase FAS2 gene from Pen  
A;Reference number: S01787; MUID:89030897; PMID:3053172  
A;Accession: S01787  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-1857 <WIE>  
A;Cross-references: UNIPROT:P15368; GB:M37461; NID:g169179; PIDN:AAA33695.1; PID:g169180  
A;Note: The source is designated as Penicillium patulum  
C;Genetics:  
A;Gene: fas2  
C;Superfamily: yeast fatty-acid synthase  
C;Keywords: acyltransferase; coenzyme A

Query Match 58.6%; Score 41; DB 1; Length 1857;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAA 13  
|:|||||  
Db 62 ASKYEAYDAATS 73

RESULT 7  
T27431  
hypothetical protein Y79HZA.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T27431  
R;Matthews, L.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20365  
A;Accession: T27431  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA



A;Residues: 1-2129 <WIL>  
A;Cross-references: UNIPROT:Q9UIR8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:Y79H2A  
A;Experimental source: clone Y79H2A  
C;Genetics:  
A;Gene: CESP:Y79H2A.3  
A;Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67/1; 1760/1; 1929/3; 2037/3; 2074/3

Query Match 58.6%; Score 41; DB 2; Length 2129;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAA 12  
| | | | | : | | |  
Db 144 EYAKYERYRSAA 155

RESULT 8  
C70521  
1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) homolog - Mycobacterium tuberculosis  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 16-Aug-2004  
C;Accession: C70521  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: C70521  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-251 <COL>  
A;Cross-references: UNIPROT:O07808; GB:Z97188; GB:AL123456; NID:G3261805; PIDN:CAB10008.  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV3815C  
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase  
C;Keywords: acyltransferase; coenzyme A

Query Match 57.1%; Score 40; DB 2; Length 251;  
Best Local Similarity 66.7%; Pred. No. 27;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAA 15  
| | | | | : | | |  
Db 229 EAAKMEADAAARA 243

RESULT 9  
GNVSR  
genome polyprotein 1 - tomato ringspot virus (strain raspberry) (fragment)  
C;Species: tomato ringspot virus  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A40787  
R;Rott, M.E.; Tremaine, J.H.; Rochon, D.M. Virology 185, 468-472, 1991  
A;Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and RNA2: evolutionary relationships  
A;Reference number: A40787; MUID:92024112; PMID:1926788  
A;Accession: A40787  
A;Molecule type: genomic RNA  
A;Residues: 1-354 <ROT>  
A;Cross-references: UNIPROT:P29150; GB:M73822; NID:G335267; PIDN:AAA47941.1; PID:G555406  
C;Genetics:  
A;Map position: segment 1  
C;Superfamily: tomato ringspot virus genome polyprotein  
C;Keywords: glycoprotein; polyprotein  
F;270/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.1%; Score 40; DB 1; Length 354;  
Best Local Similarity 57.9%; Pred. No. 38;  
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

Qy 1 EAAKYEAY----KAAAAA 15  
| | | | | : | | | | |  
Db 182 KAAYAAFAAKKAAAVAA 200

RESULT 10  
F97547  
probable oxidoreductase (PA5181) [imported] - Agrobacterium tumefaciens (strain C58, Cer  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: F97547  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: F97547  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-788 <KUR>  
A;Cross-references: UNIPROT:Q8UF51; GB:AE007869; PIDN:AAK87335.1; PID:G15156635; GSPDB:C  
C;Genetics:  
A;Gene: AGR\_C\_2854  
A;Map position: circular chromosome  
C;Superfamily: formate dehydrogenase

Query Match 57.1%; Score 40; DB 2; Length 788;  
Best Local Similarity 61.5%; Pred. No. 80;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAKYEAYKAAAA 14  
| | | | | : | | | | |  
Db 343 AAEFEAYRAAVDA 355

RESULT 11  
AC2767  
formate dehydrogenase H alpha subunit fdhF [imported] - Agrobacterium tumefaciens (strain C58)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AC2767  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E. W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AC2767  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-788 <KUR>  
A;Cross-references: UNIPROT:Q8UF51; GB:AE008688; PIDN:AAL42553.1; PID:G17739976; GSPDB:C  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: fdhF  
A;Map position: circular chromosome  
C;Superfamily: formate dehydrogenase

Query Match 57.1%; Score 40; DB 2; Length 788;  
Best Local Similarity 61.5%; Pred. No. 80;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAKYEAYKAAAA 14  
| | | | | : | | | | |  
Db 343 AAEFEAYRAAVDA 355

RESULT 12  
T13690  
hypothetical protein EG0003.2 - fruit fly (Drosophila melanogaster)



C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: T13690  
R;Murphy, L.; Harris, D.; Barrell, B.  
Submitted to the EMBL Data Library, November 1998  
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A;Reference number: Z17699  
A;Accession: T13690  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-806 <MUR>  
A;Cross-references: UNIPROT:O96828; EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA2  
C;Genetics:  
A;Cross-references: FlyBase:FBgn0025833  
A;Introns: 37/3; 448/3; 611/2; 690/3  
A;Note: EG:EG0003.2

Query Match 57.1%; Score 40; DB 2; Length 806;  
Best Local Similarity 69.2%; Pred. No. 82;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 15  
Db 743 AQYSQYAAAAAA 755  
::| | | | | | | | | |

RESULT 13  
T18535  
high molecular mass nuclear antigen - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T18535  
R;Shimada, K.; Harata, M.; Mizuno, S.  
J. Cell Sci. 110, 3031-3041, 1997  
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick  
A;Reference number: Z18955; MUID:9803440; PMID:9365273  
A;Accession: T18535  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1151 <SHI>  
A;Cross-references: UNIPROT:O57580; EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BA241

Query Match 57.1%; Score 40; DB 2; Length 1151;  
Best Local Similarity 73.3%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
Db 1100 EAAVQEAIAAAAAA 1114  
||| || | | | | | |

RESULT 14  
G75512  
conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: G75512  
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: G75512  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <WHI>  
A;Cross-references: UNIPROT:Q9RX23; GB:AE001908; GB:AE000513; NID:G6458174; PIDN:AAF1006  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR0492  
A;Map position: 1

Query Match 55.7%; Score 39; DB 2; Length 101;  
Best Local Similarity 50.0%; Pred. No. 17;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14  
Db 70 DSAHYQAYRAKAGA 83  
::| | | | | | | |

RESULT 15  
E81312  
probable lipoprotein Cj1090c [imported] - Campylobacter jejuni (strain NCTC 11168)  
C;Species: Campylobacter jejuni  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: E81312  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: E81312  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-170 <PAR>  
A;Cross-references: UNIPROT:Q9PNK4; GB:AL139077; GB:AL111168; NID:G6968444; PIDN:CAB7334E  
A;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: Cj1090c

Query Match 55.7%; Score 39; DB 2; Length 170;  
Best Local Similarity 46.7%; Pred. No. 28;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15  
Db 137 DSARYEAIRAASSEA 151  
::| | | | | | | |

Search completed: March 31, 2005, 02:42:27  
Job time : 19.9032 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds  
(without alignments)  
95.342 Million cell updates/sec

Title: US-10-056-583A-64  
Perfect score: 70  
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	65.7	847	2 Q7SC23	Q7sc23 neurospora
2	45	64.3	603	2 Q64JV8	Q64jv8 plasmodium
3	45	64.3	608	2 Q64JV9	Q64jv9 plasmodium
4	45	64.3	608	2 Q64JW1	Q64jw1 plasmodium
5	45	64.3	614	2 Q64JV2	Q64jv2 plasmodium
6	45	64.3	727	2 Q64JU8	Q64ju8 plasmodium
7	45	64.3	727	2 Q64JU3	Q64ju3 plasmodium
8	45	64.3	727	2 Q64JV7	Q64jv7 plasmodium
9	45	64.3	810	2 Q64JV4	Q64jv4 plasmodium
10	45	64.3	826	2 Q64JW3	Q64jw3 plasmodium
11	45	64.3	897	2 Q64JW5	Q64jw5 plasmodium
12	45	64.3	900	2 Q64JW4	Q64jw4 plasmodium
13	45	64.3	921	2 Q64JW1	Q64jw1 plasmodium
14	44	62.9	507	2 Q6DLT8	Q6dl8 aedes albop
15	44	62.9	509	2 Q6DLT7	Q6dl7 aedes albop
16	44	62.9	525	2 Q6DLT9	Q6dl9 aedes albop
17	44	62.9	530	2 Q6DLU0	Q6dl0 aedes aegypt
18	44	62.9	705	2 Q64JV5	Q64jv5 plasmodium
19	44	62.9	2058	2 Q6DLT4	Q6dl4 aedes albop
20	44	62.9	2064	2 Q6DLT3	Q6dl3 aedes aegypt
21	43	61.4	188	2 Q72BU7	Q72bu7 desulfovibr
22	43	61.4	395	2 Q6D7F3	Q6d7f3 erwinia car
23	42	60.0	188	1 HXD8_CHICK	P23459 gallus gall
24	42	60.0	206	2 Q87SY7	Q87sy7 vibrio para
25	42	60.0	254	1 143A_ARATH	P48347 arabidopsis
26	42	60.0	277	2 Q6ATQ0	Q6atq0 oryza sativ
27	42	60.0	289	1 HXD8_MOUSE	P23463 mus musculu
28	42	60.0	289	2 Q8IXZ1	Q8ixz1 homo sapien
29	42	60.0	290	1 HXD8_HUMAN	P13378 homo sapien
30	42	60.0	342	2 Q6ATQ1	Q6atq1 oryza sativ
31	42	60.0	380	2 Q8W0D1	Q8w0d1 oryza sativ

32	42	60.0	390	2 Q615H3	Q615h3 oryza sativ
33	42	60.0	527	1 SERA_ARCFU	O29445 archaeoglob
34	42	60.0	608	2 Q64JV6	Q64jv6 plasmodium
35	42	60.0	697	2 Q9NDJ0	Q9ndj0 plasmodium
36	42	60.0	697	2 Q64JW6	Q64jw6 plasmodium
37	42	60.0	853	2 Q7S637	Q7s637 neurospora
38	41	58.6	99	1 CU02_BLACR	P80676 blaberus cr
39	41	58.6	124	2 O82182	O82182 arabidopsis
40	41	58.6	216	2 Q95V10	Q95v10 fasciola he
41	41	58.6	415	2 Q6YWS1	Q6yws1 oryza sativ
42	41	58.6	432	2 Q81RS8	Q81rs8 drosophila
43	41	58.6	453	2 Q6AV91	Q6av91 oryza sativ
44	41	58.6	508	2 Q6QUT5	Q6qut5 corynebacte
45	41	58.6	512	2 Q7XVB8	Q7xvb8 oryza sativ

ALIGNMENTS

RESULT 1

ID	Q7SC23	PRELIMINARY;	PRT;	847 AA.
AC	Q7SC23;			
DT	01-MAR-2004 (TrEMBLrel. 26, Created)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)			
DE	Hypothetical protein.			
GN	Name=NCU08397.1;			
OS	Neurospora crassa.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.			
OX	NCBI_TaxID=5141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=OR74A;			
RA	Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,			
RA	Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,			
RA	Elkins T., Engels P., Wang S., Nielsen C.B., Butler J., Endrizzi M.,			
RA	Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,			
RA	Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,			
RA	Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,			
RA	Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,			
RA	Kamal M., Kanvyeselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,			
RA	Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,			
RA	Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,			
RA	DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,			
RA	Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,			
RA	Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,			
RA	Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;			
RT	"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";			
RL	Nature 0:0-0(2003).			
CC	-1- CAUTION: The sequence shown here is derived from an			
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is			
CC	preliminary data.			
CC	EMBL; AAEX01000143; EAA34000.1; -.			
DR	InterPro; IPR004648; Oligopept_transp.			
DR	InterPro; IPR004813; Tetrapept_transp.			
DR	Pfam; PF03169; OPT; 1			
DR	TIGRFAMs; TIGR00727; ISP4_OPT; 1.			
DR	TIGRFAMs; TIGR00728; OPT_sfam; 1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 847 AA; 94963 MW; CDAF7C5D5EFD910A CRC64;			

Query Match 65.7%; Score 46; DB 2; Length 847;

Best Local Similarity 66.7%; Pred.No. 56;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EAAKYEAYKAAAAA 15

Db 462 DAAKYEAYSPAYLAA 476

RESULT 2



```

Q64JV8
ID Q64JV8 PRELIMINARY; PRT; 603 AA.
AC Q64JV8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br781B;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PVMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454088; AAS10474.1; -.
KW Merozoite.
FT NON_TER 1
FT NON_TER 603
SQ SEQUENCE 603 AA; 65111 MW; 9FB464A42ED295C4 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 603;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 398 EAAKEEAQKAATAA 411

RESULT 3
Q64JV9
ID Q64JV9 PRELIMINARY; PRT; 608 AA.
AC Q64JV9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br67T;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PVMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454087; AAS10473.1; -.
KW Merozoite.
FT NON_TER 1
FT NON_TER 608
SQ SEQUENCE 608 AA; 65634 MW; FEC7E2627E333604 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 608;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 403 EAAKEEAQKAATAA 416

RESULT 4
Q64JW1
ID Q64JW1 PRELIMINARY; PRT; 608 AA.
AC Q64JW1;

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br56;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PVMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454085; AAS10471.1; -.
KW Merozoite.
FT NON_TER 1
FT NON_TER 608
SQ SEQUENCE 608 AA; 65845 MW; A07CDB0563F4FE03 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 608;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 403 EAAKEEAQKAATAA 416

RESULT 5
Q64JV2
ID Q64JV2 PRELIMINARY; PRT; 614 AA.
AC Q64JV2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ong;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PVMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454094; AAS10480.1; -.
KW Merozoite.
FT NON_TER 1
FT NON_TER 614
SQ SEQUENCE 614 AA; 66444 MW; 2C5C5B13F2FCBCA9 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 614;
Best Local Similarity 78.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 409 EAAKEEAQKAATAA 422

RESULT 6
Q64JU8
ID Q64JU8 PRELIMINARY; PRT; 727 AA.
AC Q64JU8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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DE Merozoite surface protein 3b (Fragment).  
OS Plasmodium vivax.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5855;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Thai;  
RX PubMed=15374528;  
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;  
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions.";  
RL Infect. Genet. Evol. 4:309-319(2004).  
DR EMBL: AY454098; AAS10484.1; -.  
KW Merozoite.  
FT NON TER 1 727  
FT NON TER 727 727  
SQ SEQUENCE 727 AA; 78545 MW; EAD28262BF32531B CRC64;  
  
Query Match 64.3%; Score 45; DB 2; Length 727;  
Best Local Similarity 78.6%; Pred. No. 71;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 EAAKYEAYKAAAA 14  
||||| |||||  
Db 522 EAAKEEAQKAATAA 535  
  
RESULT 7  
Q64JV3  
ID Q64JV3 PRELIMINARY; PRT; 727 AA.  
AC Q64JV3;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Merozoite surface protein 3b (Fragment).  
OS Plasmodium vivax.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5855;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NK;  
RX PubMed=15374528;  
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;  
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions.";  
RL Infect. Genet. Evol. 4:309-319(2004).  
DR EMBL: AY454093; AAS10479.1; -.  
KW Merozoite.  
FT NON TER 1 727  
FT NON TER 727 727  
SQ SEQUENCE 727 AA; 78556 MW; B3A309A6874F5B0D CRC64;  
  
Query Match 64.3%; Score 45; DB 2; Length 727;  
Best Local Similarity 78.6%; Pred. No. 71;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 EAAKYEAYKAAAA 14  
||||| |||||  
Db 522 EAAKEEAQKAATAA 535  
  
RESULT 8  
Q64JV7  
ID Q64JV7 PRELIMINARY; PRT; 727 AA.  
AC Q64JV7;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Merozoite surface protein 3b (Fragment).  
OS Plasmodium vivax.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=5855;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br781T;  
RX PubMed=15374528;  
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;  
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions.";  
RL Infect. Genet. Evol. 4:309-319(2004).  
DR EMBL: AY454089; AAS10475.1; -.  
KW Merozoite.  
FT NON TER 1 727  
FT NON TER 727 727  
SQ SEQUENCE 727 AA; 78668 MW; F1D764F1BB782E5C CRC64;  
  
Query Match 64.3%; Score 45; DB 2; Length 727;  
Best Local Similarity 78.6%; Pred. No. 71;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 EAAKYEAYKAAAA 14  
||||| |||||  
Db 522 EAAKEEAQKAATAA 535  
  
RESULT 9  
Q64JV4  
ID Q64JV4 PRELIMINARY; PRT; 810 AA.  
AC Q64JV4;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Merozoite surface protein 3b (Fragment).  
OS Plasmodium vivax.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5855;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=India;  
RX PubMed=15374528;  
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;  
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions.";  
RL Infect. Genet. Evol. 4:309-319(2004).  
DR EMBL: AY454092; AAS10478.1; -.  
KW Merozoite.  
FT NON TER 1 810  
FT NON TER 810 810  
SQ SEQUENCE 810 AA; 86539 MW; 14B1E39FAE44F74A CRC64;  
  
Query Match 64.3%; Score 45; DB 2; Length 810;  
Best Local Similarity 78.6%; Pred. No. 78;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 EAAKYEAYKAAAA 14  
||||| |||||  
Db 605 EAAKEEAQKAATAA 618  
  
RESULT 10  
Q64JW3  
ID Q64JW3 PRELIMINARY; PRT; 826 AA.  
AC Q64JW3;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Merozoite surface protein 3b (Fragment).  
OS Plasmodium vivax.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5855;  
RN [1]  
RP SEQUENCE FROM N.A.



```
RC STRAIN=Chess;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454083; AAS10469.1; -.
KW Merozoite.
FT NON_TER 826 826
SQ SEQUENCE 826 AA; 89752 MW; 699B1F21F5B747B6 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 826;
Best Local Similarity 78.6%; Pred. No. 80;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAA 14
DB 572 EAAKEEAQKAATAA 585

RESULT 11
Q64JW5 PRELIMINARY; PRT; 897 AA.
AC Q64JW5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br1T;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454081; AAS10467.1; -.
KW Merozoite.
FT NON_TER 897 897
SQ SEQUENCE 897 AA; 96705 MW; CB86EFCDD3CBED5EA CRC64;

Query Match 64.3%; Score 45; DB 2; Length 897;
Best Local Similarity 78.6%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAA 14
DB 643 EAAKEEAQKAATAA 656

RESULT 12
Q64JW4 PRELIMINARY; PRT; 900 AA.
AC Q64JW4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br69;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
```

```
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454082; AAS10468.1; -.
KW Merozoite.
FT NON_TER 900 900
SQ SEQUENCE 900 AA; 97231 MW; DC84487COD34BF7B CRC64;

Query Match 64.3%; Score 45; DB 2; Length 900;
Best Local Similarity 78.6%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAA 14
DB 646 EAAKEEAQKAATAA 659

RESULT 13
Q64JV1 PRELIMINARY; PRT; 927 AA.
AC Q64JV1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sal1;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454095; AAS10481.1; -.
KW Merozoite.
FT NON_TER 927 927
SQ SEQUENCE 927 AA; 99734 MW; B5DCBD6130A7F4E1 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 927;
Best Local Similarity 78.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAA 14
DB 722 EAAKEEAQKAATAA 735

RESULT 14
Q6DLT8 PRELIMINARY; PRT; 501 AA.
AC Q6DLT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Voltage-dependent para-like sodium channel (Fragment).
OS Aedes albopictus (forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7160;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu J.-H., Zhao T.-Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY663380; AAT69676.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005261; P-cation channel activity; IEA.
DR GO; GO:0006812; P-cation transport; IEA.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
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DR Pfam; PF00520; Ion trans; 2.  
KW Ion transport; Ionic channel; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 501 501  
SQ SEQUENCE 501 AA; 56497 MW; B66CD123B5EC5FDD CRC64;  
Query Match 62.9%; Score 44; DB 2; Length 501;  
Best Local Similarity 73.3%; Pred. No. 73;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 EAAKVEAYKAAAAA 15  
:|||||  
Db 76 KAALKLEAQAAAAA 90

RESULT 15  
O6DLT7 PRELIMINARY; PRT; 509 AA.  
AC O6DLT7;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Voltage-dependent para-like sodium channel (Fragment).  
OS Aedes albopictus (Forest day mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
OX NCBI\_TaxID=7160;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wu J.-H., Zhao T.-Y.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY663381; AAT69677.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005261; P:cation channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR Pfam; PF00520; Ion trans; 2.  
KW Ion transport; Ionic channel; Transmembrane; Transport.  
FT NON\_TER 1  
FT NON\_TER 509 509  
SQ SEQUENCE 509 AA; 56992 MW; 2D3DCB47D423D5C0 CRC64;  
Query Match 62.9%; Score 44; DB 2; Length 509;  
Best Local Similarity 73.3%; Pred. No. 74;  
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 EAAKVEAYKAAAAA 15  
:|||||  
Db 76 KAALKLEAQAAAAA 90

Search completed: March 31, 2005, 02:41:07  
Job time : 82.5645 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 100.629 Seconds  
(without alignments)  
65.338 Million cell updates/sec

Title: US-10-056-583A-88

Perfect score: 82

Sequence: 1 APEKAKYKAAAAA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	17	5	ABP52294 HLA-DR2 m
2	82	100.0	19	5	ABP52295 HLA-DR2 m
3	73	89.0	17	5	ABP52303 HLA-DR2 m
4	71	86.6	15	5	ABP52271 HLA-DR2 m
5	71	86.6	15	5	ABP52298 HLA-DR2 m
6	71	86.6	17	5	ABP52296 HLA-DR2 m
7	69	84.1	17	5	ABP52302 HLA-DR2 m
8	65	79.3	15	5	ABP52270 HLA-DR2 m
9	63	76.8	15	5	ABP52301 HLA-DR2 m
10	61	74.4	15	5	ABP52291 HLA-DR2 m
11	61	74.4	15	5	ABP52263 HLA-DR2 m
12	60	73.2	15	5	ABP52272 HLA-DR2 m
13	59	72.0	15	5	ABP52259 HLA-DR2 m
14	59	72.0	15	5	ABP52257 HLA-DR2 m
15	57	69.5	15	5	ABP52297 HLA-DR2 m
16	56	68.3	15	5	ABP52253 HLA-DR2 m
17	56	68.3	15	5	ABP52251 HLA-DR2 m
18	56	68.3	15	5	ABP52239 HLA-DR2 m
19	55	67.1	15	5	ABP52290 HLA-DR2 m
20	55	67.1	15	5	ABP52261 HLA-DR2 m
21	55	67.1	15	5	ABP52244 HLA-DR2 m
22	55	67.1	15	5	ABP52292 HLA-DR2 m
23	55	67.1	15	5	ABP52269 HLA-DR2 m
24	55	67.1	15	5	ABP52262 HLA-DR2 m
25	54	65.9	15	5	ABP52264 HLA-DR2 m

26	54	65.9	15	5	ABP52267 HLA-DR2 m
27	54	65.9	15	5	ABP52236 HLA-DR2 m
28	53	64.6	15	5	ABP52299 HLA-DR2 m
29	52	63.4	15	5	ABP52265 HLA-DR2 m
30	51	62.2	15	5	ABP52254 HLA-DR2 m
31	51	62.2	15	5	ABP52255 HLA-DR2 m
32	51	62.2	15	5	ABP52240 HLA-DR2 m
33	51	62.2	15	5	ABP52241 HLA-DR2 m
34	51	62.2	15	5	ABP52304 HLA-DR2 m
35	51	62.2	15	5	ABP52248 HLA-DR2 m
36	51	62.2	15	5	ABP52249 HLA-DR2 m
37	50	61.0	15	5	ABP52232 HLA-DR2 m
38	50	61.0	15	5	ABP52268 HLA-DR2 m
39	50	61.0	15	5	ABP52231 HLA-DR2 m
40	50	61.0	570	6	ADA55549 Human pro
41	50	61.0	570	7	ADJ70708 Human hea
42	49	59.8	15	5	ABP52235 HLA-DR2 m
43	49	59.8	15	5	ABP52250 HLA-DR2 m
44	48	58.5	15	5	ABP52277 HLA-DR2 m
45	48	58.5	15	5	ABP52238 HLA-DR2 m

#### ALIGNMENTS

##### RESULT 1

ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

PN 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

XX Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases



CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

XX SQ Sequence 17 AA;  
 Query Match 100.0%; Score 82; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17  
 Db 1 APEKAKYEAYKAAAAA 17  
 |||||

RESULT 2  
 ABP52295  
 ID ABP52295 standard; peptide; 19 AA.  
 XX  
 AC ABP52295;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:89.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX  
 PF 24-JAN-2001; 2001US-0263569P.  
 XX  
 PR (HARD ) HARVARD COLLEGE.  
 XX  
 PA Strominger JL, Fridkis-Hareli M;  
 XX  
 PI WPI; 2002-608439/65.  
 XX  
 DR New compositions comprising synthetic peptides in complex with a major  
 XX PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP5207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 19 AA;  
 Query Match 100.0%; Score 82; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17  
 Db 1 APEKAKYEAYKAAAAA 17  
 |||||

RESULT 3  
 ABP52303  
 ID ABP52303 standard; peptide; 17 AA.  
 XX  
 AC ABP52303;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:97.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX  
 PF 24-JAN-2001; 2001US-0263569P.  
 XX  
 PR (HARD ) HARVARD COLLEGE.  
 XX  
 PA Strominger JL, Fridkis-Hareli M;  
 XX  
 PI WPI; 2002-608439/65.  
 XX  
 DR New compositions comprising synthetic peptides in complex with a major  
 XX PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 17 AA;  
 Query Match 89.0%; Score 73; DB 5; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.7e-05;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17



```

Db      1 APEKAFAYKAAAAA 17
|||||:|||||
RESULT 4
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match      86.6%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      3 EKAKYEAYKAAAAA 17
Db      1 EKAKYEAYKAAAAA 15
|||||:|||||
RESULT 6
ABP52296
ID ABP52296 standard; peptide; 17 AA.
XX
AC ABP52296;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
XX

```



KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN WO200259143-A2.  
 XX  
 XX 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX  
 XX 24-JAN-2001; 2001US-0263569P.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX  
 XX Strominger JL, Fridkis-Hareli M;  
 XX WPI; 2002-608439/65.  
 XX  
 XX New compositions comprising synthetic peptides in complex with a major  
 XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
 XX encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 AA;  
 Query Match 86.6%; Score 71; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.0001;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 EKAKYEAYKAAATAA 17  
 Db 1 EKAKYEAYKAAATAA 15  
 RESULT 7  
 ABP52302  
 ID ABP52302 standard; peptide; 17 AA.  
 XX  
 AC ABP52302;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 XX 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 XX  
 XX 24-JAN-2001; 2001US-0263569P.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX  
 XX Strominger JL, Fridkis-Hareli M;  
 XX WPI; 2002-608439/65.  
 XX  
 XX New compositions comprising synthetic peptides in complex with a major  
 XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 XX demyelinating disease, e.g. multiple sclerosis, or post-viral  
 XX encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 AA;  
 Query Match 84.1%; Score 69; DB 5; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 0.00021;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 APEKAYEAYKAAATAA 17  
 Db 1 APEKAYEAYKAAATAA 17  
 RESULT 8  
 ABP52270  
 ID ABP52270 standard; peptide; 15 AA.  
 XX  
 AC ABP52270;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:64.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 XX 01-AUG-2002.  
 XX







XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX SQ Sequence 15 AA;

Query Match 74.4%; Score 61; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0039;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17

Db 1 EKPKYEAYKAAAAA 15

RESULT 11

ABP52263

ID ABP52263 standard; peptide; 15 AA.

XX AC ABP52263;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:57.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX Example 1; Page 33; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX SQ Sequence 15 AA;

Query Match 74.4%; Score 61; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0039;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17

Db 1 EEAKYAAYKAAAAA 15

RESULT 12

ABP52272

ID ABP52272 standard; peptide; 15 AA.

XX AC ABP52272;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:66.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to



CC ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 73.2%; Score 60; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0057; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | |  
DB 1 EAKYEAYKAAAAA 15

RESULT 13  
ABP52259  
ID ABP52259 standard; peptide; 15 AA.  
XX  
AC ABP52259;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:53.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.  
XX  
XX Example 1; Page 33; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has anti-inflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX  
SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0083;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | |  
DB 1 EAKYEAYKAAAAA 15

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | |  
DB 1 EAKYEAYKAAAAA 15

RESULT 14  
ABP52257  
ID ABP52257 standard; peptide; 15 AA.  
XX  
AC ABP52257;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.  
XX  
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.  
XX  
XX Example 1; Page 32; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has anti-inflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX  
SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0083;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | | | | | | |  
DB 1 EAKYEAYKAAAAA 15



RESULT 15  
 ABP52297  
 ID ABP52297 standard; peptide; 15 AA.  
 XX  
 AC ABP52297;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:91.  
 XX  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX WFI; 2002-608439/65.  
 XX  
 DR New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;

Query Match 69.5%; Score 57; DB 5; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 0.018;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 EKAKYEAYKAAAAA 17  
 |||:|||||||  
 Db 1 EKPKFEAYKAAAAA 15

Search completed: March 31, 2005, 02:35:27  
 Job time : 100.629 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 26.0484 Seconds  
(without alignments)  
48.718 Million cell updates/sec

Title: US-10-056-583A-88  
Perfect score: 82  
Sequence: 1 APEKAYEYKAAAAA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	53.7	596	2	US-08-836-620A-16
2	43	52.4	162	4	US-09-732-210-1445
3	43	52.4	324	4	US-09-248-796A-17156
4	42	51.2	13	5	PCT-US95-04121-38
5	42	51.2	190	4	US-09-902-540-14713
6	42	51.2	273	4	US-09-910-430-34
7	42	51.2	1001	4	US-09-248-796A-18658
8	41	50.0	402	4	US-09-248-796A-17859
9	40	48.8	13	5	PCT-US94-10257A-33
10	40	48.8	56	4	US-09-405-743A-3
11	40	48.8	56	4	US-09-816-989A-3
12	40	48.8	77	4	US-09-405-743A-5
13	40	48.8	77	4	US-09-816-989A-5
14	40	48.8	86	4	US-09-405-743A-6
15	40	48.8	86	4	US-09-816-989A-6
16	40	48.8	109	4	US-09-405-743A-7
17	40	48.8	109	4	US-09-816-989A-7
18	40	48.8	466	4	US-09-489-039A-13950
19	40	48.8	802	4	US-09-489-039A-11230
20	40	48.8	1156	4	US-09-198-452A-171
21	40	48.8	1562	4	US-09-438-185A-152
22	39	47.6	38	3	US-09-117-121-16
23	39	47.6	38	3	US-09-117-121-24
24	39	47.6	38	4	US-09-344-529-5
25	39	47.6	166	4	US-09-252-991A-22139
26	39	47.6	202	4	US-09-205-258-344
27	39	47.6	219	4	US-09-902-540-16623

28	39	47.6	309	4	US-09-107-532A-6391	Sequence 6391, Ap
29	39	47.6	411	4	US-09-248-796A-18456	Sequence 18456, A
30	39	47.6	497	1	US-08-295-670-6	Sequence 6, Appli
31	39	47.6	497	1	US-08-633-485-6	Sequence 6, Appli
32	39	47.6	510	3	US-08-508-761B-4	Sequence 4, Appli
33	39	47.6	601	4	US-09-252-991A-21824	Sequence 21824, A
34	39	47.6	731	4	US-09-252-991A-18769	Sequence 18769, A
35	38.5	47.0	459	4	US-09-543-681A-5116	Sequence 5116, Ap
36	38	46.3	54	3	US-09-117-121-30	Sequence 30, Appli
37	38	46.3	163	2	US-08-245-511-2	Sequence 2, Appli
38	38	46.3	163	2	US-08-600-993A-2	Sequence 2, Appli
39	38	46.3	171	4	US-10-144-198-28	Sequence 28, Appli
40	38	46.3	186	4	US-09-902-540-11242	Sequence 11242, A
41	38	46.3	319	4	US-09-270-767-45793	Sequence 45793, A
42	38	46.3	333	4	US-09-198-452A-652	Sequence 652, App
43	38	46.3	335	4	US-09-438-185A-615	Sequence 615, App
44	38	46.3	351	4	US-09-489-039A-7442	Sequence 7442, Ap
45	38	46.3	391	4	US-09-328-352-4861	Sequence 4861, Ap

ALIGNMENTS

RESULT 1  
US-08-836-620A-16  
; Sequence 16, Application US/08836620A  
; Patent No. 5958710  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Orphan receptor  
; NUMBER OF SEQUENCES: 19  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836.620A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP96/03933  
; FILING DATE:  
; APPLICATION NUMBER: GB 9518272.1  
; FILING DATE: 08-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9605550.4  
; FILING DATE: 15-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9607532.0  
; FILING DATE: 11-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9609576.5  
; FILING DATE: 08-MAY-1996  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 596 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus rattus  
US-08-836-620A-16

Query Match 53.7%; Score 44; DB 2; Length 596;  
Best Local Similarity 68.8%; Pred. No. 28;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PEKAYEYKAAAAA 17  
Db 55 PEGAAEFNAAAAA 70

RESULT 2  
US-09-732-210-1445



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; Sequence 1445, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1445
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-732-210-1445

Query Match          52.4%; Score 43; DB 4; Length 162;
Best Local Similarity 52.9%; Pred. No. 9.9;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
Db 97 AKPSKLEVFNAALAAA 113

RESULT 3
US-09-248-796A-17156
; Sequence 17156, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17156
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17156

Query Match          52.4%; Score 43; DB 4; Length 324;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAA 14
Db 157 APEKAKESAPAAA 170

RESULT 4
PCT-US95-04121-38
; Sequence 38, Application PC/TUS9504121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
; NUMBER OF SEQUENCES: 62
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04121
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/222,206
; APPLICATION NUMBER:
; FILING DATE: April 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 079.2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-38

Query Match          51.2%; Score 42; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.93;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAAA 17
Db 1 AAYKAKAAAAAA 13

RESULT 5
US-09-902-540-14713
; Sequence 14713, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14713
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14713

Query Match          51.2%; Score 42; DB 4; Length 190;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAA 14
Db 120 APERTEYVWRAAA 133

RESULT 6
US-09-910-430-34
; Sequence 34, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
```



```
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-34

Query Match      51.2%; Score 42; DB 4; Length 273;
Best Local Similarity 52.9%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy      1 APEKAKYEAYKAAAAA 17
Db      203 APAVASYQTYHAAPAVA 219

RESULT 7
US-09-248-796A-18658
; Sequence 18658, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18658
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18658

Query Match      51.2%; Score 42; DB 4; Length 1001;
Best Local Similarity 78.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 KAKYEAYKAAAAA 17
Db      818 KAKEEAEEAAAAA 831

RESULT 8
US-09-248-796A-17859
; Sequence 17859, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
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; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17859
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17859

Query Match      50.0%; Score 41; DB 4; Length 402;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 KAKYEAYKAA 13
Db      70 KAKYESYDAA 79

RESULT 9
PCT-US94-10257A-33
; Sequence 33, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEK
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US94-10257A-33

Query Match      48.8%; Score 40; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5 AKYEAYKAAAAA 17
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Db 1 AAYAAKAAAAA 13

```

RESULT 10
US-09-405-743A-3
; Sequence 3, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-3
SYNTHETIC

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Query Match 48.8%; Score 40; DB 4; Length 56;  
Best Local Similarity 60.0%; Pred. No. 9.7;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy            1 APEKAKVEAYKAAA 15  
               | :|: :||| |  
Db            18 AAKEAEAKYKAAEA 32

```

RESULT 11
US-09-816-989A-3
; Sequence 3, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3

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Query Match 48.8%; Score 40; DB 4; Length 56;  
Best Local Similarity 60.0%; Pred. No. 9.7;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy            1 APEKAKVEAYKAAA 15  
               | : | : : | | |  
Db            18 AAKKAEAKYKAAEA 32

RESULT 12  
US-09-405-743A-5  
; Sequence 5, Application US/09405743A  
; Patent No. 6514938

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; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-5
SYNTHETIC

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Query Match	48.8%	Score 40;	DB 4;	Length 77;
Best Local Similarity	60.0%	Pred. No. 14;		
Matches	9;	Conservative	3;	Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 APEKAKYEAYKAAA 15
        | : | : | : | : |
Db     18 AAKKAEAKYKAAEA 32
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```

RESULT 13
US-09-816-989A-5
/ Sequence 5, Application US/09816989A
/ Patent No. 6800287
/ GENERAL INFORMATION:
/ APPLICANT: Gad, Alexander
/ APPLICANT: Lie, Doris
/ TITLE OF INVENTION: COPOLYMER 1 REL
/ TITLE OF INVENTION: AND FOR THERAP
/ FILE REFERENCE: 2609/50807-A-PCT-US
/ CURRENT APPLICATION NUMBER: US/09/8
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/101,693
/ PRIOR FILING DATE: 1998-09-25
/ PRIOR APPLICATION NUMBER: PCT/US99/
/ PRIOR FILING DATE: 1999-09-24
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 5
/ LENGTH: 77
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of 1
US-09-816-989A-5

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Query Match	48.8%	Score 40;	DB 4;	Length 77;
Best Local Similarity	60.0%;	Pred. No. 14;		
Matches 9;	Conservative	3;	Mismatches	3;
			Indels	0;
			Gaps	0;

Qy . 1 APEKAKVEAYKAAA 15  
| : | : | : | : |  
pb 18 AAKEAEAKYKAFAA 32

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RESULT 14
US-09-405-743A-6
; Sequence 6, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
US-09-405-743A-6

Query Match 48.8%; Score 40; DB 4; Length 86;  
Best Local Similarity 60.0%; Pred. No. 15;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAA 15  
| :||: :|||  
Db 18 AAKKAEAKAYKAAEA 32

RESULT 15  
US-09-816-989A-6  
; Sequence 6, Application US/09816989A  
; Patent No. 6800287  
; GENERAL INFORMATION:  
; APPLICANT: Gad, Alexander  
; APPLICANT: Lis, Doris  
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK  
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE  
; FILE REFERENCE: 2609/60807-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/816,989A  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/101,693  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: PCT/US99/22402  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide  
US-09-816-989A-6

Query Match 48.8%; Score 40; DB 4; Length 86;  
Best Local Similarity 60.0%; Pred. No. 15;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAA 15  
| :||: :|||  
Db 18 AAKKAEAKAYKAAEA 32

Search completed: March 31, 2005, 02:44:08  
Job time : 27.0484 secs



**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 75.4032 Seconds  
(without alignments)  
74.648 Million cell updates/sec

Title: US-10-056-583A-88

Perfect score: 82  
Sequence: 1 APEKAKYEAYKAAAAA 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	17	14 US-10-056-583-88	Sequence 88, Appl
2	82	100.0	19	14 US-10-056-583-89	Sequence 89, Appl
3	73	89.0	17	14 US-10-056-583-97	Sequence 97, Appl
4	71	86.6	15	14 US-10-056-583-65	Sequence 65, Appl
5	71	86.6	17	14 US-10-056-583-90	Sequence 90, Appl
6	69	84.1	17	14 US-10-056-583-96	Sequence 96, Appl
7	65	79.3	15	14 US-10-056-583-64	Sequence 64, Appl
8	63	76.8	15	14 US-10-056-583-95	Sequence 95, Appl
9	62	75.6	15	14 US-10-056-583-92	Sequence 92, Appl
10	61	74.4	15	14 US-10-056-583-57	Sequence 57, Appl
11	61	74.4	15	14 US-10-056-583-85	Sequence 85, Appl
12	60	73.2	15	14 US-10-056-583-66	Sequence 66, Appl
13	59	72.0	15	14 US-10-056-583-51	Sequence 51, Appl

14	72.0	15	14	US-10-056-583-53	Sequence 53, Appl
15	69.5	15	14	US-10-056-583-91	Sequence 91, Appl
16	68.3	15	14	US-10-056-583-33	Sequence 33, Appl
17	68.3	15	14	US-10-056-583-45	Sequence 45, Appl
18	68.3	15	14	US-10-056-583-47	Sequence 47, Appl
19	67.1	15	14	US-10-056-583-38	Sequence 38, Appl
20	67.1	15	14	US-10-056-583-55	Sequence 55, Appl
21	67.1	15	14	US-10-056-583-56	Sequence 56, Appl
22	67.1	15	14	US-10-056-583-63	Sequence 63, Appl
23	67.1	15	14	US-10-056-583-84	Sequence 84, Appl
24	67.1	15	14	US-10-056-583-86	Sequence 86, Appl
25	65.9	15	14	US-10-056-583-30	Sequence 30, Appl
26	65.9	15	14	US-10-056-583-58	Sequence 58, Appl
27	65.9	15	14	US-10-056-583-61	Sequence 61, Appl
28	64.6	15	14	US-10-056-583-93	Sequence 93, Appl
29	63.4	15	14	US-10-056-583-59	Sequence 59, Appl
30	62.2	15	14	US-10-056-583-34	Sequence 34, Appl
31	62.2	15	14	US-10-056-583-35	Sequence 35, Appl
32	62.2	15	14	US-10-056-583-42	Sequence 42, Appl
33	62.2	15	14	US-10-056-583-43	Sequence 43, Appl
34	62.2	15	14	US-10-056-583-48	Sequence 48, Appl
35	62.2	15	14	US-10-056-583-49	Sequence 49, Appl
36	62.2	15	14	US-10-056-583-98	Sequence 98, Appl
37	61.0	15	14	US-10-056-583-25	Sequence 25, Appl
38	61.0	15	14	US-10-056-583-26	Sequence 26, Appl
39	61.0	15	14	US-10-056-583-62	Sequence 62, Appl
40	61.0	570	15	US-10-094-749-3117	Sequence 3117, Ap
41	61.0	570	16	US-10-408-765A-2514	Sequence 2514, Ap
42	59.8	15	14	US-10-056-583-29	Sequence 29, Appl
43	59.8	15	14	US-10-056-583-44	Sequence 44, Appl
44	58.5	15	14	US-10-056-583-32	Sequence 32, Appl
45	58.5	15	14	US-10-056-583-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1  
US-10-056-583-88  
; Sequence 88, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-88

Query Match 100.0%; Score 82; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APEKAKYEAYKAAAAA 17  
Db 1 APEKAKYEAYKAAAAA 17

RESULT 2  
US-10-056-583-89



```
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match 100.0%; Score 82; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKYEAYKAAAAA 17
```

```
RESULT 3
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match 89.0%; Score 73; DB 14; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKFEAYKAAAP 17
```

```
RESULT 4
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match 86.6%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 5
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match 86.6%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```



```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match      84.1%; Score 69; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00021;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKFEAFKAAAAA 17

RESULT 7
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

Query Match      79.3%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00081;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKYEAYKAAAAA 17
Db 1 EAKYEAYKAAAAA 15

RESULT 8
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match      76.8%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0017;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EKAKYEAYKAAAAA 17
Db 1 EKAKFEAFKAAAAA 15

RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match      75.6%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0025;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EKAKYEAYKAAAAA 17
Db 1 EKAKYEAYKAAAAA 15

RESULT 10
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```



OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-57

Query Match 74.4%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0036;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
DB 1 EAKYAAYKAAAAA 15

RESULT 11  
US-10-056-583-85  
; Sequence 85, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-85

Query Match 74.4%; Score 61; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0036;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
DB 1 EKPKYEAYKAAAAA 15

RESULT 12  
US-10-056-583-66  
; Sequence 66, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 73.2%; Score 60; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0052;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
DB 1 EAKKYEAYKAAAAA 15

RESULT 13  
US-10-056-583-51  
; Sequence 51, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 72.0%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0076;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
DB 1 EAKYAAYKAAAAA 15

RESULT 14  
US-10-056-583-53  
; Sequence 53, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-53

Query Match 72.0%; Score 59; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.0076;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17  
DB 1 EAKYAAYKAAAAA 15



RESULT 15  
US-10-056-583-91  
; Sequence 91, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-91

Query Match 69.5%; Score 57; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.016;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKYEAYKAAAAA 17  
| | | | | | | | | |  
Db 1 EKPKFEAYKAAAAA 15

Search completed: March 31, 2005, 02:48:48  
Job time : 75.4032 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 31, 2005, 02:26:17 ; Search time 20.2903 Seconds  
(without alignments)  
80.614 Million cell updates/sec

Title: US-10-056-583A-88  
Perfect score: 82  
Sequence: 1 APEKAKYEAYKAAAAA 17  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	54.9	154	2 H81076	conserved hypothet
2	45	54.9	154	2 B81866	conserved hypothet
3	45	54.9	179	2 F97683	50S ribosomal prot
4	45	54.9	179	2 A29008	50S ribosomal prot
5	44.5	54.3	189	2 S77930	exoskeletal protei
6	44.5	54.3	189	2 S77935	exoskeletal protei
7	44	53.7	599	1 QRMSE	estrogen receptor
8	44	53.7	600	1 QRRTE	estrogen receptor
9	43	52.4	162	2 H70927	probable rpsP prot
10	43	52.4	185	2 S36290	T-cell receptor ga
11	43	52.4	347	2 A81794	probable rotamase
12	43	52.4	348	2 B81216	peptidyl-prolyl ci
13	43	52.4	421	2 JV0057	tolA protein - Esc
14	43	52.4	441	2 A43555	GAP-43-related pro
15	42	51.2	188	2 I50145	homeotic protein H
16	42	51.2	289	2 A43562	homeotic protein H
17	42	51.2	329	2 D96030	hypothetical prote
18	42	51.2	1167	2 D97516	DNA polymerase III
19	42	51.2	1167	2 AD2735	DNA polymerase III
20	41	50.0	88	2 JC2184	transcription fact
21	41	50.0	129	1 TNLJG3	trans-activating t
22	41	50.0	177	2 AD1307	peptidyl methionin
23	41	50.0	177	2 AD1679	peptidyl methionin
24	41	50.0	254	2 H86355	probable 14-3-3 pr
25	41	50.0	289	2 AC1399	hypothetical prote
26	41	50.0	641	2 PH1919	Flu-160-4 protein -
27	41	50.0	1885	1 JC4086	fatty-acid synthas
28	41	50.0	2129	2 T27431	hypothetical prote
29	40	48.8	73	2 S40015	phd protein - phag

30	40	48.8	75	2 S61806	M-like protein enn
31	40	48.8	106	1 TNLJS2	trans-activating t
32	40	48.8	107	2 AB3271	hypothetical prote
33	40	48.8	202	2 A83492	probable transcrip
34	40	48.8	377	2 T43037	probable fatty-aci
35	40	48.8	467	2 AC2015	hypothetical prote
36	40	48.8	478	2 S04675	H+-transporting tw
37	40	48.8	480	2 G70302	conserved hypothet
38	40	48.8	594	2 T50013	hypothetical prote
39	40	48.8	806	2 T13690	hypothetical prote
40	40	48.8	829	2 E64114	translation initia
41	40	48.8	1537	2 P86509	CT147 hypothetica
42	40	48.8	1537	2 C81558	conserved hypothet
43	40	48.8	1537	2 H72112	CT147 hypothetica
44	40	48.8	1842	2 T43409	probable fatty-aci
45	40	48.8	1842	2 T38781	fatty acid synthas

ALIGNMENTS

RESULT 1

H81076  
conserved hypothetical protein NMB1500 [imported] - Neisseria meningitidis (strain MCS8)  
C:Species: Neisseria meningitidis  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: H81076  
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masigiani, V.; Pizzazi, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: H81076  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-154 <TET>  
A:Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:g7226737; PIDN:AAF4185  
A:Experimental source: serogroup B, strain MCS8  
C:Genetics:  
A:Gene: NMB1500  
C:Superfamily: Escherichia coli ybdQ protein

Query Match 54.9%; Score 45; DB 2; Length 154;  
Best Local Similarity 56.2%; Pred. No. 5.4;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APEKAKYEAYKAAAAA 16  
||| :|:|:|:|  
Db 48 APEFLQESYEAAAAVA 63

RESULT 2

B81866  
conserved hypothetical protein NMA1703 [imported] - Neisseria meningitidis (strain Z2491)  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: B81866  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
F.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: B81866  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-154 <PAR>  
A:Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1703  
C:Superfamily: Escherichia coli ybdQ protein



```

Query Match      54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 5.4;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 16
    |||:::|:|:|
Db 48 APEFLOHESYEAAVA 63

RESULT 3
F97683
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97683
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F97683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <KUR>
A:Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:G15157917; GSPDB:C
C:Genetics:
A:Gene: AGR_C 4900
A:Map position: circular chromosome
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match      54.9%; Score 45; DB 2; Length 179;
Best Local Similarity 64.7%; Pred. No. 6.3;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
    |||:::|:|:|
Db 135 ABEKARLEAEKVAAAAA 151

RESULT 4
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2908
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2908
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-179 <KUR>
A:Cross-references: UNIPROT:Q8UBZ5; GB:AF008688; PIDN:AAAL43684.1; PID:G17741210; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: rplS
A:Map position: circular chromosome
C:Superfamily: Escherichia coli ribosomal protein L19

Query Match      54.9%; Score 45; DB 2; Length 179;
Best Local Similarity 64.7%; Pred. No. 6.3;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
    |||:::|:|:|
Db 135 ABEKARLEAEKVAAAAA 151

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RESULT 5
S77930
exoskeletal protein HACP202A - American lobster (fragment)
C:Species: Homarus americanus (American lobster)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S77930
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus
A:Reference number: S77925
A:Accession: S77930
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-189 <NOU>
A:Cross-references: UNIPROT:Q7M496

Query Match      54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 8;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 APEKAK-YEAYKAAAAAA 17
    |||:::|:|:|
Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 6
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C:Species: Homarus americanus (American lobster)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S77935
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus
A:Reference number: S77925
A:Accession: S77935
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-189 <NOU>
A:Cross-references: UNIPROT:Q7M495

Query Match      54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 8;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 APEKAK-YEAYKAAAAAA 17
    |||:::|:|:|
Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 7
QRMSE
estrogen receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: A40061
R:White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A:Title: Structural organization and expression of the mouse estrogen receptor.
A:Reference number: A40061; MUID:91042558; PMID:2484714
A:Accession: A40061
A:Molecule type: mRNA
A:Residues: 1-599 <WHI>
A:Cross-references: UNIPROT:P19785; GB:M38651; PIDN:AAA37580.1; PID:G193180
C:Comment: The steroid hormones and their receptors are involved in the regulation of eu
C:Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
C:Superfamily: estrogen receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
C:KeyWords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept
F;1-183/Domain: amino-terminal <NH2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-460/Domain: erba transforming protein homology <ERBA>

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100



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Db      15 APOKAKTASAKAKAA 30
      ||:||| : ||| ||
      15 APOKAKTASAKAKAA 30

RESULT 12
B81216
peptidyl-prolyl, cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (strain
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81216
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiognani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81216
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <LET>
A;Cross-references: UNIPROT:Q9K186; GB:AE002385; GB:AE002098; NID:G7225506; PIDN:AAF4073
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0281

Query Match      52.4%; Score 43; DB 2; Length 348;
Best Local Similarity 52.5%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY      1 APEKAKYEAYKAAAA 16
      ||:||| : ||| ||
      22 APOKAKTASAKAKAA 37

Db      22 APOKAKTASAKAKAA 37

RESULT 13
JV0057
tola protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levensgood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tola and tolB genes and localization of their produ
A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
A;Molecule type: DNA
A;Residues: 1-421 <LEV>
A;Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97456617; PMID:9278503
A;Accession: B64810
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AACT3833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tola and tolB proteins are necessary for collins E2, E3, A, and K to reach b
C;Genetics:
A;Gene: tola
A;Map position: 17 min
A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
F;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)

Query Match      52.4%; Score 43; DB 2; Length 421;

```

```

Best Local Similarity 73.3%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAA 15
      ||:||| : ||| ||
      215 AAEKAKAEAEKAAAA 229

Db      215 AAEKAKAEAEKAAAA 229

RESULT 14
A43555
GAP-43-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43555; S65398
R;Ng, S.C.; Perkins, L.A.; Conboy, G.; Perrimon, N.; Fishman, M.C.
Development 105, 629-638, 1989
A;Title: A Drosophila gene expressed in the embryonic CNS shares one conserved domain wit
A;Reference number: A43555; MUID:90126372; PMID:2693037
A;Accession: A43555
A;Molecule type: mRNA
A;Residues: 1-441 <NGA>
A;Cross-references: UNIPROT:P29746; EMBL:X63828
R;Perkins, L.A.
submitted to the EMBL Data Library, December 1991
A;Reference number: S65398
A;Accession: S65398
A;Molecule type: mRNA
A;Residues: 1-111, 'AIPKTKL', 120, 'ERAK', 125, 'AOENA', 131, 'VEAKKQKTKTARTE', 146, 'EPTVEAQP', 1
A;Cross-references: EMBL:X63828; NID:g7663; PID:g7664
A;Note: the differences in residues 112-178 are due to frameshift errors
C;Genetics:
A;Gene: FlyBase:bnb
A;Cross-references: FlyBase:FBgn0001090
A;Map position: 10

Query Match      52.4%; Score 43; DB 2; Length 441;
Best Local Similarity 58.8%; Pred. No. 32;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAA 17
      ||:||| : ||| ||
      263 APEKKSIESPPAAAAAS 279

Db      263 APEKKSIESPPAAAAAS 279

RESULT 15
I50145
homeotic protein Hox M - chicken
N;Alternate names: CHOX M
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: I50145; S14512
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic virus
A;Reference number: I50145; MUID:91238215; PMID:1674560
A;Accession: I50145
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <CRO>
A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701
C;Genetics:
A;Gene: CHOX M
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>

Query Match      51.2%; Score 42; DB 2; Length 188;
Best Local Similarity 81.8%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 YEAYKAAAAAA 17
      ||:||| : ||| ||
      10 YSKYKAAAAAA 20

Db      10 YSKYKAAAAAA 20

```



Search completed: March 31, 2005, 02:42:28  
Job time : 21.2903 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: March 31, 2005, 02:18:02 ; Search time 91.3065 Seconds  
(without alignments)  
95.342 Million cell updates/sec

Title: US-10-056-583A-88

Perfect score: 82

Sequence: 1 APEKAKYEYKAAAAA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	61.0	570	2	Q96M46
2	48	58.5	707	2	Q64CP3
3	45	54.9	154	2	Q9JTN1
4	45	54.9	154	2	Q9JYN4
5	45	54.9	179	1	RL19_AGR75
6	45	54.9	300	2	Q9VFL4
7	45	54.9	375	2	Q75GC3
8	45	54.9	395	2	Q6D7F3
9	45	54.9	463	2	Q9V7U6
10	44.5	54.3	189	2	Q7M495
11	44.5	54.3	189	2	Q7M496
12	44	53.7	113	2	Q6LAN9
13	44	53.7	272	2	Q9P7P0
14	44	53.7	306	2	Q69J37
15	44	53.7	316	2	Q8A8P1
16	44	53.7	574	2	Q8XW8
17	44	53.7	599	1	ESR1_MOUSE
18	44	53.7	600	1	ESR1_RAT
19	44	53.7	607	2	Q9W327
20	43	52.4	162	1	R316_MYCBO
21	43	52.4	162	1	R316_MYCTU
22	43	52.4	289	2	Q71W13
23	43	52.4	299	1	RL222_DROME
24	43	52.4	304	2	Q7S9P3
25	43	52.4	312	2	Q9UAN1
26	43	52.4	319	2	Q9N603
27	43	52.4	319	2	Q9NG86
28	43	52.4	319	2	Q9NG87
29	43	52.4	319	2	Q9NG88
30	43	52.4	319	2	Q9NG89
31	43	52.4	319	2	Q9NG90

Q89J65 bradyrhizob  
Q9JEP0 neisseria m  
Q9K186 neisseria m  
Q8EHS3 shewanella  
Q83SAL shigella fl  
P19934 escherichia  
Q8FJT1 escherichia  
P29746 drosophila  
Q6GUT5 corynebacte  
Q7SGF5 neurospora  
Q6CCF1 yarrowia li  
Q7S6Z8 neurospora  
Q8BYX1 mus musculus  
Q6X3F6 pseudomonas

#### ALIGNMENTS

RESULT 1

Q96M46  
ID Q96M46 PRELIMINARY; PRT; 570 AA.  
AC Q96M46;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein FLJ32830.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,  
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Toghiani T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
cDNAs";  
RL Nat. Genet. 36:40-45 (2004).  
RL EMBL; AK057392; BAB71466.1; -.  
DR InterPro; IPR008938; ARM.  
SQ SEQUENCE 570 AA; 65769 MW; 65BEB6F244FC7E2 CRC64;

Query Match 61.0%; Score 50; DB 2; Length 570;

Best Local Similarity 69.2%; Pred.No. 17;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;



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QY      2 PEKAKYEAYKAAA 14
Db      194 PEKYEAYRTLA 206

RESULT 2
Q64CP3
ID Q64CP3 PRELIMINARY; PRT; 707 AA.
AC Q64CP3;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ1D1.21;
OS uncultured archaeon GZfoslD1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AY174833; AAU82834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match 58.5%; Score 48; DB 2; Length 707;
Best Local Similarity 70.6%; Pred. No. 43;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAA 17
Db      643 AAEKIKSEAEKAAAA 659

RESULT 3
Q9JTN1
ID Q9JTN1 PRELIMINARY; PRT; 154 AA.
AC Q9JTN1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA1703.
GN OrderedLocNames=NMA1703;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RC MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Dehavin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
RW EMBL; AL162756; CAB84931.1; -.
DR PIR; B81866; B81866.
DR HSSP; P44880; 1JMV.
DR GO; GO:0006950; P:response to stress; IEA.

QY      2 PEKAKYEAYKAAA 14
Db      194 PEKYEAYRTLA 206

Query Match 54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAA 16
Db      48 APEFLQHSYEAAVA 63

RESULT 5
RL19 AGRT5
ID RL19 AGRT5 STANDARD; PRT; 179 AA.
AC Q8UBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

```



DE 50S ribosomal protein L19.  
GN Name=rplS; OrderedLocusNames=Atu2703, AGR\_C.4900;  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
OX NCBI\_TaxID=176299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Kutyavint T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
RT C58.";  
RL Science 294:2317-2323(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Qurrello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
RA Houmle K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,  
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
RT Agrobacterium tumefaciens C58.";  
RL Science 294:2323-2328(2001).  
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit  
CC interface and may play a role in the structure and function of the  
CC aminoacyl-tRNA binding site [by similarity].  
CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
CC -----  
DR EMBL; AB009216; AAL43684.1; -;  
DR EMBL; AB008183; AAK88423.1; -;  
DR PIR; AF2908; AF2908.  
DR PIR; F97683; F97683.  
DR HMAP; MF 00402; -; 1.  
DR InterPro; IPR001857; Ribosomal\_L19.  
DR Pfam; PF01245; Ribosomal\_L19; 1.  
DR PRINTS; PR00061; Ribosomal\_L19.  
DR ProDom; PD002979; Ribosomal\_L19; 1.  
DR TIGRfam; TIGR01024; rplS\_bact; 1.  
DR PROSITE; PS01015; RIBOSOMAL\_L19; 1.  
KW Complete proteome; Ribosomal protein.  
SQ SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;  
Query Match 54.9%; Score 45; DB 1; Length 179;  
Best Local Similarity 64.7%; Pred. No. 35;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Oy 1 APEKAKYEYKAAAAAA 17  
| | | | | | | | | |  
Db 135 AEEKARLEAEKVAQAQA 151  
RESULT 6  
Q9VFL4 PRELIMINARY; PRT; 300 AA.  
ID Q9VFL4

AC Q9VFL4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE CG14840-PA (AT18408p).  
DE ORFNames=CG14840;  
GN Drosophila melanogaster (Fruit fly).  
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Basley E.M.,  
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fowler C., Gabriellian A.C., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shier B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spive E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scher S.E., Myers S.E., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnik S.E.,  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).



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[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003704; AAF55038.1; -.
DR EMBL; AY089356; AAL90094.1; -.
DR IntAct; Q9VFL4; -.
DR FlyBase; FBGN0038217; CG14840.
DR InterPro; IPR007995; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;

Query Match 54.9%; Score 45; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 16
Db 242 EKTQAAAYKAAACA 255

RESULT 7
ID Q75GC3 PRELIMINARY; PRT; 375 AA.
AC Q75GC3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Expressed protein, having alternative splicing products (Putative RNA
DE pol II accessory factor) (With alternative splicing).
GN Names=OSJNB0031A14.2; Synonyms=OSJNBa0034D21.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN 1
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.

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RA Buell R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC145387; AAR8603.1; -.
DR EMBL; AC137991; AAS07322.1; -.
SQ SEQUENCE 375 AA; 42035 MW; 3B060F30076D2264 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 375;
Best Local Similarity 58.8%; Pred. No. 70;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 17
Db 178 APSSARHEPSSAAAAA 194

RESULT 8
ID Q6D7F3 PRELIMINARY; PRT; 395 AA.
AC Q6D7F3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ToLA protein.
GN Name=ToLA; OrderedLocustNames=ECA1372;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaiha M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Praser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG74282.1; -.
DR InterPro; IPR010528; ToLA.
DR Pfam; PF06519; ToLA; 1.
KW Complete proteome.
SQ SEQUENCE 395 AA; 41698 MW; 2DB1DAA64E984199 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 395;
Best Local Similarity 70.6%; Pred. No. 74;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAYEAYKAAAAA 17
Db 203 AAETAKAEAKAAAEAA 219

RESULT 9
ID Q9V7U6 PRELIMINARY; PRT; 463 AA.
AC Q9V7U6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```



DE CG6301-PA.  
GN ORFNames=CG6301;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003805; AAF57947.2; -;  
DR IntAct; Q9V706; -;  
DR FlyBase; FBgn0034161; CG6301.  
DR InterPro; IPR007999; DUF745.  
DR Pfam; PF05335; DUF745; 1.  
SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEF6BEC9 CRC64;  
Query Match 54.9%; Score 45; DB 2; Length 463;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 EKAKYEAYKAAAA 16  
Db 275 ETKQAAYKAAACA 288  
RESULT 10  
Q7M495 Q7M495 PRELIMINARY; PRT; 189 AA.  
AC Q7M495;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Exoskeletal protein HACP202B (Fragment).  
OS Homarus americanus (American lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Nephropoidea; Nephropidae; Homarus.  
OC NCBI\_TaxID=6706;  
RN [1]  
RP SEQUENCE.  
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;  
RL Submitted (JUN-1997) to the PIR data bank.  
DR PIR; S77935; S77935.  
FT NON TER 1 1  
FT NON TER 189 189  
SQ SEQUENCE 189 AA; 20180 MW; 72A4EFD9C7ECFE9 CRC64;  
Query Match 54.3%; Score 44.5; DB 2; Length 189;  
Best Local Similarity 61.1%; Pred. No. 44;  
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
Qy 1 APEKAK-YEAYKAAAAA 17  
Db 9 AAEKARFFQAFKAAENAA 26  
RESULT 11  
Q7M496 Q7M496 PRELIMINARY; PRT; 189 AA.  
AC Q7M496;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Exoskeletal protein HACP202A (Fragment).  
OS Homarus americanus (American lobster).



```

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL Submitted (JUN-1997) to the PIR data bank.
RA PIR: S77930; S77930.. 1
FT NON_TER 189
FT NON_TER 189
SQ SEQUENCE 189 AA; 20154 MW; 72A4EFC9C647FE9 CRC64;

Query Match 54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 44;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 1 APEKAK-YEAYKAAAAA 17
| | | | : | | | | |
Db 9 AA EKARPFQAFKAAAAA 26
| | | | : | | | | |

RESULT 12
Q6LAN9 PRELIMINARY; PRT; 113 AA.
AC Q6LAN9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Estrogen receptor protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Freyschues B., Grandien K.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: X98236; CAA66888.1; --
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0005496; F:steroid binding; IEA.
DR GO: GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001292; Oestrgn_receptor.
DR Pfam: PF02159; Oest_recep; 1.
DR PRINTS; PR00543; OESTROGENR.
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 11671 MW; A820B1196B918387 CRC64;

Query Match 53.7%; Score 44; DB 2; Length 113;
Best Local Similarity 68.8%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PEKAYEAYKAAAAA 17
| | | | : | | | | |
Db 55 PEGAYEAFNAAAAA 70
| | | | : | | | | |

RESULT 13
Q8P7P0 PRELIMINARY; PRT; 272 AA.
AC Q8P7P0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein XCC2571.
GN OrderedLocusNames=XCC2571;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

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OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Melandris J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AE012368; AAM41843.1; --
DR GO: GO:0005524; F:ATP binding; IEA.
DR InterPro: IPR000808; Mrp.
DR PROSITE; PS01215; Mrp; 1.
DR Complete proteome.
SQ SEQUENCE 272 AA; 28377 MW; 1713145CEC084925 CRC64;

Query Match 53.7%; Score 44; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APEKAYEAYKAAAA 15
| | | | : | | | | |
Db 237 APESAAAQAYLAAAA 251
| | | | : | | | | |

RESULT 14
Q69J37 PRELIMINARY; PRT; 306 AA.
AC Q69J37;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNBa0072106.16 (Hypothetical protein
DE P0493C06.31).
GN Name=OSJNBa0072106.16; Synonyms=P0493C06.31;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OSJNBa0072106.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0493C06.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP006458; BAD32025.1; --
DR EMBL: AP005193; BAD31146.1; --
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0030001; F:metal ion transport; IEA.
DR InterPro: IPR006121; HeavyWe_transpt.
KW Hypothetical protein.

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SQ SEQUENCE 306 AA; 32378 MW; A60288C9B77E868 CRC64;  
Query Match 53.7%; Score 44; DB 2; Length 306;  
Best Local Similarity 68.8%; Pred. No. 84;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAAA 17  
| | | : | | | | |  
Db 122 PEKAAKADKAAAAA 137

## RESULT 15

Q8A8P1 PRELIMINARY; PRT; 316 AA.  
AC Q8A8P1;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Mobilization protein BmgA.  
GN OrderedLocusNames=Btl126;  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."  
RL Science 299:2074-2076(2003).  
DR EMBL; AE016930; AA076233.1; -.  
DR InterPro; IPR005094; Relaxase.  
DR Pfam; PF03432; Relaxase; 1.  
KW Complete proteome.  
SQ SEQUENCE 316 AA; 36130 MW; B63E149ACEDEC898 CRC64;

Query Match 53.7%; Score 44; DB 2; Length 316;  
Best Local Similarity 56.2%; Pred. No. 86;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 16  
| | | | | : | | | |  
Db 171 ASEKVKYEIVRAVKEA 186

Search completed: March 31, 2005, 02:41:09  
Job time : 93.3065 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds  
(without alignments)  
65.338 Million cell updates/sec

Title: US-10-056-583A-91

Perfect score: 76

Sequence: 1 EXPFEAYKAAAPA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No.	Score	Query			DB ID	Description
		Match	Length	DB		
1	76	100.0	15	5	ABP52297	HLA-DR2 m
2	73	96.1	15	5	ABP52291	HLA-DR2 m
3	70	92.1	15	5	ABP52304	HLA-DR2 m
4	69	90.8	15	5	ABP52299	HLA-DR2 m
5	68	89.5	17	5	ABP52303	HLA-DR2 m
6	67	88.2	15	5	ABP52290	HLA-DR2 m
7	67	88.2	15	5	ABP52292	HLA-DR2 m
8	64	84.2	17	5	ABP52302	HLA-DR2 m
9	63	82.9	15	5	ABP52300	HLA-DR2 m
10	63	82.9	15	5	ABP52305	HLA-DR2 m
11	57	75.0	15	5	ABP52271	HLA-DR2 m
12	57	75.0	15	5	ABP52289	HLA-DR2 m
13	57	75.0	15	5	ABP52298	HLA-DR2 m
14	57	75.0	17	5	ABP52294	HLA-DR2 m
15	57	75.0	17	5	ABP52296	HLA-DR2 m
16	57	75.0	19	5	ABP52295	HLA-DR2 m
17	56	73.7	15	5	ABP52301	HLA-DR2 m
18	53	69.7	15	5	ABP52293	HLA-DR2 m
19	53	69.7	781	8	ADN60395	B. lichen
20	53	69.7	781	8	ADN60505	B. lichen
21	53	69.7	781	8	ADN60519	B. lichen
22	51	67.1	15	5	ABP52270	HLA-DR2 m
23	51	67.1	15	5	ABP52272	HLA-DR2 m
24	47	61.8	15	5	ABP52263	HLA-DR2 m
25	46	60.5	299	4	ABB63276	Drosophil

26	46	60.5	299	8	ADS96704	Ad96704 Drosophil
27	45	59.2	15	5	ABP52264	HLA-DR2 m
28	45	59.2	15	5	ABP52267	HLA-DR2 m
29	45	59.2	15	5	ABP52259	HLA-DR2 m
30	45	59.2	15	5	ABP52257	HLA-DR2 m
31	44	57.9	377	6	ABU23345	Protein e
32	43	56.6	15	5	ABP52265	HLA-DR2 m
33	43	56.6	336	6	ABP79775	N. gonorr
34	43	56.6	336	6	ABU38057	Protein e
35	43	56.6	336	6	ABU37170	Protein e
36	43	56.6	336	8	ADP08309	Neisseria
37	43	56.6	572	4	ABB5072	Drosophil
38	42	55.3	15	5	ABP52254	HLA-DR2 m
39	42	55.3	15	5	ABP52255	HLA-DR2 m
40	42	55.3	15	5	ABP52240	HLA-DR2 m
41	42	55.3	15	5	ABP52253	HLA-DR2 m
42	42	55.3	15	5	ABP52251	HLA-DR2 m
43	42	55.3	15	5	ABP52241	HLA-DR2 m
44	42	55.3	15	5	ABP52249	HLA-DR2 m
45	42	55.3	15	5	ABP52239	HLA-DR2 m

ALIGNMENTS

RESULT 1

ABP52297  
ID ABP52297 standard; peptide; 15 AA.  
XX  
AC ABP52297;  
XX  
DT 16-OCT-2002 (first entry)  
XX  
DB HLA-DR2 molecule binding peptide SEQ ID NO:91.  
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PD 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

XX Strominger JL, Fridkis-Hareli M;  
WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a  
XX demyelinating disease, e.g. multiple sclerosis, or post-vital  
XX encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
XX residues. The complex of the peptide with a major histocompatibility  
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an  
XX immune response. (I) has antiinflammatory and neuroprotective activities,  
XX and can be used as a MHC class II protein inhibitor. The compositions  
XX comprising the peptides are useful for treating demyelinating diseases



CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

XX Sequence 15 AA;

Query Match 100.0%; Score 76; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
 |||||  
 DB 1 EKPKEAYKAAAPAA 15

## RESULT 2

ABP52291  
 ID ABP52291 standard; peptide; 15 AA.

XX  
 AC ABP52291;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:85.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 15 AA;

Query Match 96.1%; Score 73; DB 5; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 4.3e-05;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15  
 |||||  
 DB 1 EKPKEAYKAAAPAA 15

## RESULT 3

ABP52304

ID ABP52304 standard; peptide; 15 AA.

XX  
 AC ABP52304;

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:98.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

PF 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

PA (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

DR WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 15 AA;

Query Match 92.1%; Score 70; DB 5; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 0.00013;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15



RESULT 5  
ABP52303  
ID ABP52303



KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 PF  
 XX 24-JAN-2001; 2001US-0263569P.  
 PR  
 XX (HARD ) HARVARD COLLEGE.  
 PA  
 XX Strominger JL, Fridkis-Hareli M;  
 PI  
 XX WPI; 2002-608439/65.  
 DR  
 XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (II) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 88.2%; Score 67; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.00042;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EKPKEAYKAAAPA 15  
 DB 1 EAPKYEAYKAAAPA 15  
 |||:|||||||  
 RESULT 7  
 ABP52292  
 ID ABP52292 standard; peptide; 15 AA.  
 XX  
 AC ABP52292;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:86.  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 XX 24-JAN-2002; 2002WO-US002071.  
 PF  
 XX 24-JAN-2001; 2001US-0263569P.  
 PR  
 XX (HARD ) HARVARD COLLEGE.  
 PA  
 XX Strominger JL, Fridkis-Hareli M;  
 PI  
 XX WPI; 2002-608439/65.  
 DR  
 XX New compositions comprising synthetic peptides in complex with a major  
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
 PT encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (II) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 88.2%; Score 67; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.00042;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EKPKEAYKAAAPA 15  
 DB 1 EAPKYEAYKAAAPA 15  
 |||:|||||||  
 RESULT 8  
 ABP52302  
 ID ABP52302 standard; peptide; 17 AA.  
 XX  
 AC ABP52302;  
 XX  
 DT 16-OCT-2002 (first entry)  
 XX  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 XX  
 PD 01-AUG-2002.  
 XX



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PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
XX encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 17 AA;
SQ
Query Match 84.2%; Score 64; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKFEAYKAAAPAA 15
DB 3 EKAKFEAFKAAAPAA 17
RESULT 9
ABP52300
ID ABP52300 standard; peptide; 15 AA.
XX
XX
AC ABP52300;
XX
XX 16-OCT-2002 (first entry).
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:94.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 82.9%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKFEAYKAAAPAA 15
DB 1 EKPKFEAFKAAAPAA 15
RESULT 10
ABP52305
ID ABP52305 standard; peptide; 15 AA.
XX
XX
AC ABP52305;
XX
XX 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:99.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

```



XX Claim 28; Page 39; 54pp; English.

PS The present invention describes compositions (I) comprising a peptide

XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX SQ Sequence 15 AA;

Query Match 82.9%; Score 63; DB 5; Length 15;

Best Local Similarity 86.7%; Pred. No. 0.0019; 2; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 2;

QY 1 EKPKFEAYKAAAPAA 15

DB 1 EAPKVEAYKAAAPAA 15

RESULT 11

ABP52271

ID ABP52271 standard; peptide; 15 AA.

XX HLA-DR2 molecule binding peptide SEQ ID NO:65.

AC ABP52271;

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PD 24-JAN-2002; 2002WO-US002071.

PF 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

PS New compositions comprising synthetic peptides in complex with a major

XX histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

PS The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

XX immune response. (I) has antiinflammatory and neuroprotective activities,

XX and can be used as a MHC class II protein inhibitor. The compositions

XX comprising the peptides are useful for treating demyelinating diseases

XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

XX demyelinating condition, and a side effect of administering an anti-

XX tumour necrosis factor agents. The peptide further inhibits proliferation

XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

XX ABP52305 represent peptides used in the exemplification of the present

XX invention

XX SQ Sequence 15 AA;

Query Match 75.0%; Score 57; DB 5; Length 15;

Best Local Similarity 80.0%; Pred. No. 0.019; 2; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 2;

QY 1 EKPKFEAYKAAAPAA 15

DB 1 EKAKVEAYKAAAPAA 15

RESULT 12

ABP52289

ID ABP52289 standard; peptide; 15 AA.

XX HLA-DR2 molecule binding peptide SEQ ID NO:83.

AC ABP52289;

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX immune response; antiinflammatory; neuroprotective; proliferation;

XX MHC class II protein inhibitor; demyelinating disease; inhibition;

XX post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX anti-tumour necrosis factor agent.

OS Homo sapiens.

OS Synthetic.

PN WO200259143-A2.

XX 01-AUG-2002.

PD 24-JAN-2002; 2002WO-US002071.

PF 24-JAN-2001; 2001US-0263569P.

XX (HARD ) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

PS New compositions comprising synthetic peptides in complex with a major

XX histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

PS The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

XX immune response. (I) has antiinflammatory and neuroprotective activities,

XX and can be used as a MHC class II protein inhibitor. The compositions

XX comprising the peptides are useful for treating demyelinating diseases

XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

XX demyelinating condition, and a side effect of administering an anti-

XX tumour necrosis factor agents. The peptide further inhibits proliferation

XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

XX ABP52305 represent peptides used in the exemplification of the present

XX invention



CC ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 75.0%; Score 57; DB 5; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.019;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
| : : : : :  
Db 1 EAPAYKAYKAAAPAA 15

RESULT 13  
ABP52298  
ID ABP52298 standard; peptide; 15 AA.  
XX  
AC ABP52298;  
XX  
XX 16-OCT-2002 (first entry)  
XX HLA-DR2 molecule binding peptide SEQ ID NO:92.  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agent. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 75.0%; Score 57; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.019;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
| : : : : :  
Db 1 EKAKYEAYKAAAPAA 15

RESULT 14  
ABP52294  
ID ABP52294 standard; peptide; 17 AA.  
XX  
AC ABP52294;  
XX  
XX 16-OCT-2002 (first entry)  
XX HLA-DR2 molecule binding peptide SEQ ID NO:88.  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
XX  
PD 01-AUG-2002.  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX Strominger JL, Fridkis-Hareli M;  
XX WPI; 2002-608439/65.  
XX  
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.  
XX  
PS Claim 28; Page 39; 54pp; English.  
XX  
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agent. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 17 AA;

Query Match 75.0%; Score 57; DB 5; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.021;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
| : : : : :  
Db 3 EKAKYEAYKAAAPAA 17



RESULT 15	
ABP52296	
ID	ABP52296 standard; peptide; 17 AA.
XX	
XX	ABP52296;
XX	
XX	16-OCT-2002 (first entry)
DT	
XX	
DE	HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX	
KW	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW	immune response; antiinflammatory; neuroprotective; proliferation;
KW	MHC class II protein inhibitor; demyelinating disease; inhibition;
KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW	anti-tumour necrosis factor agent.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200259143-A2.
XX	
PD	01-AUG-2002.
XX	
XX	24-JAN-2002; 2002WO-US002071.
PF	
XX	
PR	24-JAN-2001; 2001US-0263569P.
XX	
PA	(HARD ) HARVARD COLLEGE.
XX	
FI	Strominger JL, Fridkis-Hareli M;
XX	
DR	WPI; 2002-608439/65.
XX	
PT	New compositions comprising synthetic peptides in complex with a major
PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT	demyelinating disease, e.g. multiple sclerosis, or post-viral
PT	encephalomyelitis.
XX	
PS	Claim 28; Page 39; 54pp; English.
XX	
CC	The present invention describes compositions (I) comprising a peptide
CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC	residues. The complex of the peptide with a major histocompatibility
CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC	immune response. (I) has antiinflammatory and neuroprotective activities,
CC	and can be used as a MHC class II protein inhibitor. The compositions
CC	comprising the peptides are useful for treating demyelinating diseases
CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC	demyelinating condition, and a side effect of administering an anti-
CC	tumour necrosis factor agents. The peptide further inhibits proliferation
CC	of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC	ABP52305 represent peptides used in the exemplification of the present
CC	invention
XX	
SQ	Sequence 17 AA;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds  
(without alignments)  
48.718 Million cell updates/sec

Title: US-10-056-583A-91  
Perfect score: 76  
Sequence: 1 EKPFEAYKAAAPA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	52.6	2471	1	US-08-185-432-16
2	40	52.6	2471	1	US-08-083-590A-19
3	40	52.6	2471	1	US-08-532-384-19
4	40	52.6	2471	4	US-08-899-232-1
5	40	52.6	2471	4	US-09-121-457-1
6	39	51.3	75	4	US-09-513-999C-5101
7	39	51.3	222	4	US-09-949-016-9547
8	39	51.3	243	4	US-09-489-039A-7214
9	39	51.3	297	4	US-09-252-991A-18932
10	39	51.3	314	3	US-09-004-838-14
11	39	51.3	469	4	US-09-252-991A-27869
12	39	51.3	1402	3	US-09-004-838-11
13	38	50.0	66	4	US-09-902-540-16512
14	38	50.0	203	4	US-09-248-796A-20648
15	38	50.0	260	4	US-09-248-796A-17592
16	38	50.0	287	3	US-09-105-697-7
17	38	50.0	287	3	US-09-105-697-8
18	38	50.0	288	3	US-09-105-697-3
19	38	50.0	291	3	US-09-105-697-4
20	38	50.0	291	3	US-09-105-697-5
21	38	50.0	291	3	US-09-105-697-6
22	38	50.0	435	4	US-09-949-016-7245
23	38	50.0	490	4	US-10-029-180-76
24	38	50.0	499	4	US-09-902-540-15480
25	38	50.0	576	4	US-09-543-681A-7747
26	38	50.0	830	1	US-07-977-434-6
27	38	50.0	830	1	US-08-458-819-6

28	38	50.0	830	5	PCT-US91-07035-6	Sequence 6, Appli
29	38	50.0	831	1	US-08-073-384C-5	Sequence 5, Appli
30	38	50.0	831	1	US-08-254-359A-5	Sequence 5, Appli
31	38	50.0	831	1	US-08-483-043-5	Sequence 5, Appli
32	38	50.0	831	1	US-08-481-238-5	Sequence 5, Appli
33	38	50.0	831	2	US-08-471-066B-5	Sequence 5, Appli
34	38	50.0	831	2	US-08-484-956-5	Sequence 5, Appli
35	38	50.0	831	2	US-08-757-653-5	Sequence 5, Appli
36	38	50.0	831	2	US-08-599-491-5	Sequence 5, Appli
37	38	50.0	831	2	US-08-756-386-5	Sequence 5, Appli
38	38	50.0	831	2	US-08-823-516-5	Sequence 5, Appli
39	38	50.0	831	3	US-08-682-853A-5	Sequence 5, Appli
40	38	50.0	831	3	US-08-759-038-5	Sequence 5, Appli
41	38	50.0	831	3	US-08-758-314-5	Sequence 5, Appli
42	38	50.0	831	3	US-09-350-309-5	Sequence 5, Appli
43	38	50.0	831	3	US-08-520-946-5	Sequence 5, Appli
44	38	50.0	831	4	US-09-684-938-5	Sequence 5, Appli
45	38	50.0	831	4	US-09-308-825A-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-185-432-16  
; Sequence 16, Application US/08185432  
; Patent No. 5750652  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Busseau, Isabelle  
; APPLICANT: Diederich, Robert J.  
; APPLICANT: Xu, Tian  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08185,432  
; FILING DATE: 21-JAN-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2471 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-185-432-16

Query Match 52.6%; Score 40; DB 1; Length 2471;  
Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 EKPFEAYKAAAP 14



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Db      850 ESPNFESYTCCLCAP 863
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RESULT 2
US-08-083-590A-19
; Sequence 19, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-083-590A-19

Query Match      52.6%; Score 40; DB 1; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 EKPKFEAYKAAAP 14
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Db      850 ESPNFESYTCCLCAP 863
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RESULT 3
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-083-590A-19

Query Match      52.6%; Score 40; DB 1; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 EKPKFEAYKAAAP 14
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Db      850 ESPNFESYTCCLCAP 863
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RESULT 4
US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-899-232-1

Query Match      52.6%; Score 40; DB 4; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 EKPKFEAYKAAAP 14
      ||| ||| |||
Db      850 ESPNFESYTCCLCAP 863
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RESULT 5
US-09-121-457-1
; Sequence 1, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
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; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-1

Query Match          52.6%; Score 40; DB 4; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EKPKEAYKAAAP 14
Db 850 ESPNFESYTCLCAP 863

RESULT 6
US-09-513-999C-5101
; Sequence 5101, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5101
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5101

Query Match          51.3%; Score 39; DB 4; Length 75;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPKFEAYKAAAP 15
Db 7 EPKKEAAKPAPAP 20

RESULT 7
US-09-949-016-9547
; Sequence 9547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9547
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9547

Query Match          51.3%; Score 39; DB 4; Length 222;
Best Local Similarity 64.3%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPKFEAYKAAAP 15
Db 32 EPKKEAAKPAPAP 45

RESULT 8
US-09-489-039A-7214
; Sequence 7214, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7214
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7214

Query Match          51.3%; Score 39; DB 4; Length 243;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KPKFEAYKAAAP 14
Db 122 PEFTAFSAATP 133

RESULT 9
US-09-252-991A-18932
; Sequence 18932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18932
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18932

Query Match          51.3%; Score 39; DB 4; Length 297;
Best Local Similarity 46.7%; Pred. No. 52;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKPKEAYKAAAP 15
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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKPKEAYKAA 11  
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Db 515 EKPKEAYKAA 525

## RESULT 13

US-09-902-540-16512  
; Sequence 16512, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 16512

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-16512

Query Match 50.0%; Score 38; DB 4; Length 66;

Best Local Similarity 72.7%; Pred. No. 15;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FEAYKAAAPAA 15  
|||||:  
Db 48 FEYAAALAAPA 58

## RESULT 14

US-09-248-796A-20648

; Sequence 20648, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; PRIOR FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 20648

; LENGTH: 203

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (11)

; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno

US-09-248-796A-20648

Query Match 50.0%; Score 38; DB 4; Length 203;

Best Local Similarity 77.8%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KPKFEAYKAA 10  
|||||:  
Db 42 KPKFPPTYKA 50

## RESULT 15

US-09-248-796A-17592

; Sequence 17592, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17592

; LENGTH: 260

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-17592

Query Match 50.0%; Score 38; DB 4; Length 260;

Best Local Similarity 87.5%; Pred. No. 67;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PKPEAYKA 10  
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Db 112 PKPEAYKA 119

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds  
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74.648 Million cell updates/sec

Title: US-10-056-583A-91

Perfect score: 76  
Sequence: 1 EKPKFEAYKAAAPAA 15Scoring table: BLOSUM62  
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Searched: 1407402 seqs, 331100923 residues

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Maximum Match 100%

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- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	14	US-10-056-583-91
2	73	96.1	15	14	Sequence 91, Appl
3	70	92.1	15	14	Sequence 85, Appl
4	69	90.8	15	14	Sequence 98, Appl
5	68	89.5	17	14	Sequence 93, Appl
6	67	88.2	15	14	Sequence 97, Appl
7	67	88.2	15	14	Sequence 84, Appl
8	64	84.2	17	14	Sequence 86, Appl
9	63	82.9	15	14	Sequence 96, Appl
10	63	82.9	15	14	Sequence 94, Appl
11	57	75.0	15	14	Sequence 99, Appl
12	57	75.0	15	14	Sequence 65, Appl
13	57	75.0	17	14	Sequence 83, Appl
					Sequence 88, Appl

14	75.0	17	14	US-10-056-583-90	Sequence 90, Appl
15	75.0	19	14	US-10-056-583-89	Sequence 89, Appl
16	73.7	15	14	US-10-056-583-95	Sequence 95, Appl
17	69.7	15	14	US-10-056-583-87	Sequence 87, Appl
18	67.1	15	14	US-10-056-583-64	Sequence 64, Appl
19	67.1	15	14	US-10-056-583-66	Sequence 66, Appl
20	67.1	15	14	US-10-056-583-92	Sequence 92, Appl
21	61.8	15	14	US-10-056-583-57	Sequence 57, Appl
22	59.2	15	14	US-10-056-583-51	Sequence 51, Appl
23	59.2	15	14	US-10-056-583-53	Sequence 53, Appl
24	59.2	15	14	US-10-056-583-58	Sequence 58, Appl
25	59.2	15	14	US-10-056-583-61	Sequence 61, Appl
26	57.9	377	15	US-10-282-122A-51269	Sequence 51269, A
27	56.6	15	14	US-10-056-583-59	Sequence 59, Appl
28	56.6	336	15	US-10-282-122A-65094	Sequence 65094, A
29	56.6	336	15	US-10-282-122A-65981	Sequence 65981, A
30	55.9	316	16	US-10-767-701-45123	Sequence 45123, A
31	55.3	15	14	US-10-056-583-33	Sequence 33, Appl
32	55.3	15	14	US-10-056-583-34	Sequence 34, Appl
33	55.3	15	14	US-10-056-583-35	Sequence 35, Appl
34	55.3	15	14	US-10-056-583-43	Sequence 43, Appl
35	55.3	15	14	US-10-056-583-45	Sequence 45, Appl
36	55.3	15	14	US-10-056-583-47	Sequence 47, Appl
37	55.3	15	14	US-10-056-583-48	Sequence 48, Appl
38	55.3	15	14	US-10-056-583-49	Sequence 49, Appl
39	53.9	15	14	US-10-056-583-38	Sequence 38, Appl
40	53.9	15	14	US-10-056-583-55	Sequence 55, Appl
41	53.9	15	14	US-10-056-583-56	Sequence 56, Appl
42	53.9	15	14	US-10-056-583-62	Sequence 62, Appl
43	53.9	15	14	US-10-056-583-63	Sequence 63, Appl
44	53.9	317	15	US-10-310-154-522	Sequence 522, App
45	53.9	319	16	US-10-767-701-47195	Sequence 47195, A

## ALIGNMENTS

RESULT 1  
US-10-056-583-91  
; Sequence 91, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-91

Query Match 100.0%; Score 76; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15

Db 1 EKPKFEAYKAAAPAA 15

RESULT 2

US-10-056-583-85



```

; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

```

```

Query Match          96.1%; Score 73; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.2e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EKPKEAYKAAAPAA 15
   |||||
Db 1 EKPKEAYKAAAPAA 15

```

```

RESULT 3
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98

```

```

Query Match          92.1%; Score 70; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EKPKEAYKAAAPAA 15
   |||||
Db 1 EAPKEAYKAAAPAA 15

```

```

RESULT 4
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.

```

```

; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93

```

```

Query Match          90.8%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EKPKEAYKAAAPAA 15
   |||||
Db 1 EKPKEAYKAAAPAA 15

```

```

RESULT 5
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

```

```

Query Match          89.5%; Score 68; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 EKPKEAYKAAAPAA 15
   |||||
Db 3 EKAKPEAYKAAAPAA 17

```

```

RESULT 6
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583

```



; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-84

Query Match 88.2%; Score 67; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 9e-05;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
|||:|||||  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 7  
US-10-056-583-86  
; Sequence 86, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 86  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-86

Query Match 88.2%; Score 67; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 9e-05;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
|||:|||||  
Db 1 EAPKYEAYKAAAPAA 15

RESULT 8  
US-10-056-583-96  
; Sequence 96, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 96  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-96

Query Match 84.2%; Score 64; DB 14; Length 17;  
Best Local Similarity 86.7%; Pred. No. 0.00034;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
|||:|||||  
Db 3 EKAKFEAFKAAAPAA 17

RESULT 9  
US-10-056-583-94  
; Sequence 94, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 94  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-94

Query Match 82.9%; Score 63; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.00044;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15  
|||:|||||  
Db 1 EKPKFEAFKAAAPAA 15

RESULT 10  
US-10-056-583-99  
; Sequence 99, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 99  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:



; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-99

Query Match 82.9%; Score 63; DB 14; Length 15;  
Best Local Similarity 86.7%; Pred. No. 0.00044;  
Matches 13; Conservative 0; Mismatches 2; Indels

Qy 1 EKPKFEAYKAAAAA 15  
| | | | | | | | | |  
Db 1 EAPKVEAYKAAAAA 15

RESULT 11

```

US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Ströminger, Jack L.
; APPLICANT: Fridkiss-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-65

```

Query Match 75.0%; Score 57; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0048;  
Matches 12; Conservative 1; Mismatches 2; Indels

Qy 1 EKPKFEAYKAAAAA 15  
|||:|||||  
Db 1 EKAKYEAYKAAAAA 15

## RESULT 12

```

US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkies-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-83

```

Query Match	75.0%	Score 57;	DB 14;	Length 15;
Best Local Similarity	73.3%	Pred. No. 0.0048;		

Matches	11;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy 1 EKPKFEAYKAAAAA 15  
| | | | | | | | | |  
Db 1 EAPAYKAYKAAAAA 15

## RESULT 13

```

US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-88

```

Query Match 75.0%; Score 57; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0056;  
Matches 12; Conservative 1; Mismatches 2; Indels

Qy 1 EKPFEAYKAAAAA 15  
|||:|||||  
Db 3 EKAKYEAYKAAAAA 17

## RESULT 14

```

US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

```

Query Match 75.0%; Score 57; DB 14; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0056;  
Matches 12; Conservative 1; Mismatches 2; Indels

Qy 1 EKPKFEAYKAAAAA 15  
|||:|||||||  
Db 1 EKAKYEAYKAAAAA 15



RESULT 15  
US-10-056-583-89  
; Sequence 89, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; CURRENT FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-89

Query Match 75.0%; Score 57; DB 14; Length 19;  
Best Local Similarity 80.0%; Pred. No. 0.0063;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EKPKEAYKAAAPA 15  
|||:|||||  
Db 3 EKAYEAYKAAAAA 17

Search completed: March 31, 2005, 02:48:48  
Job time : 66.5323 secs



**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds  
(without alignments)  
80.614 Million cell updates/sec

Title: US-10-056-583A-91

Perfect score: 76  
Sequence: 1 EKPFEEYKAAAPAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	57.9	193	1 MOWS4E	myosin alkali ligh
2	43	56.6	306	2 G96014	hypothetical prote
3	43	56.6	336	2 B81081	cryptophanyl-tRNA li
4	43	56.6	336	2 E81863	cryptophanyl-tRNA li
5	43	56.6	389	2 G87332	hypothetical prote
6	42.5	55.9	316	2 T14643	1-aminocyclopropan
7	42	55.3	270	2 T31225	traF protein homol
8	42	55.3	554	2 S68365	(+)-delta-cadinene
9	42	55.3	554	2 S68366	(+)-delta-cadinene
10	41	53.9	185	1 MOWH4E	myosin alkali ligh
11	41	53.9	193	1 MOWT4E	myosin alkali ligh
12	41	53.9	194	2 T14644	1-aminocyclopropan
13	41	53.9	200	2 T48130	hypothetical prote
14	41	53.9	216	2 AG3508	transporter BME120
15	41	53.9	398	2 T21061	hypothetical prote
16	40	52.6	321	2 T07922	probable 1-aminocy
17	40	52.6	461	2 A13358	pyruvate dehydroge
18	40	52.6	765	2 T15447	hypothetical prote
19	40	52.6	891	2 AC3384	ribonuclease E / z
20	39	51.3	73	2 S40015	phd protein - phag
21	39	51.3	114	2 G81353	hypothetical prote
22	39	51.3	168	2 A45943	vitelline membrane
23	39	51.3	197	1 MOWH4E	myosin alkali ligh
24	39	51.3	215	2 AG3392	maleylpyruvate iso
25	39	51.3	239	1 C44954	fumarate reductase
26	39	51.3	310	2 T09733	1-aminocyclopropan
27	39	51.3	321	2 T02754	probable 1-aminocy
28	39	51.3	334	1 D5QYG	glyceraldehyde-3-p
29	39	51.3	334	2 E75153	glyceraldehyde 3-p

30	39	51.3	334	2 G71194	probable glycerald
31	39	51.3	337	1 C70473	phosphate-binding
32	39	51.3	465	2 D83598	probable zinc prot
33	39	51.3	538	2 S54015	C-22 sterol desatu
34	39	51.3	586	2 T29657	hypothetical prote
35	39	51.3	656	2 A51479	probable cell surf
36	39	51.3	810	2 C95401	probable oxidoredu
37	38.5	50.7	906	2 T00039	hypothetical prote
38	38	50.0	50	2 G97151	50S ribosomal prot
39	38	50.0	179	2 P97683	50S ribosomal prot
40	38	50.0	179	2 AF2908	homeotic protein H
41	38	50.0	188	2 T50145	ABC transporter AT
42	38	50.0	269	2 E86691	homeotic protein H
43	38	50.0	289	2 A43562	1-aminocyclopropan
44	38	50.0	308	2 T10817	hypothetical prote
45	38	50.0	320	2 B86255	hypothetical prote

ALIGNMENTS

RESULT 1

MOWS4E

myosin alkali light chain 4, embryonic and atrial - mouse

N:Alternate names: MLC1A; MLC1emb; myosin LI catalytic light chain, atrial

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004

C:Accession: A31114; S01944

R:Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Sassoon, D.; Weydert, A.; Buckingha

J. Biol. Chem. 263, 12669-12676, 1988

A:Title: Structure and sequence of the myosin alkali light chain gene expressed in adult

A:Reference number: A31114; MUID:88315068; PMID:2842339

A:Accession: A31114

A:Molecule type: DNA

A:Residues: 1-193 <BAR>

A:Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:G199731; PIDN:A

R:Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.

Nucleic Acids Res. 16, 10037-10052, 1988

A:Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striate

A:Reference number: S01944; MUID:89057447; PMID:3194193

A:Accession: S01944

A:Molecule type: DNA

A:Residues: 1-41 <COH>

A:Cross-references: EMBL:X12971; NID:G53138; PIDN:CAA31414.1; PID:G53139

C:Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet

C:Genetics:

A:Introns: 41/3; 51/1; 101/1; 159/1; 185/1

C:Superfamily: calmodulin; calmodulin repeat homology

C:Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contrac

F:47-81/Domain: calmodulin repeat homology <EF1>

F:126-158/Domain: calmodulin repeat homology <EF3>

F:161-193/Domain: calmodulin repeat homology <EF4>

Query Match 57.9%; Score 44; DB 1; Length 193;

Best Local Similarity 71.4%; Pred. No. 4;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 KPKEEYKAAAPAA 15

Db 7 EPKKEAAKPAAPAA 20

RESULT 2

G96014

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymb

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C:Accession: G96014

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: G96014







```
Matches 10; Conservative 4; Mismatches 1; Indels 3; Gaps 1;
QY 1 EKPFEAYKAAA---APA 15
   ::||| ||| :||
Db 298 KEPEAVKAAAPKSSPA 315

RESULT 7
TJ1225
traf protein homolog - Sphingomonas aromaticivorans plasmid pNL1
C:Species: Sphingomonas aromaticivorans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: TJ1225
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
submitted to the EMBL Data Library, July 1998
A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
A:Reference number: Z20992
A:Accession: TJ1225
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-270 <ROM>
A:Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:G3378261; PID:G3378366; PIDN:AAD0
C:Genetics:
A:Genome: plasmid pNL1
A:Note: traf

Query Match 55.3%; Score 42; DB 2; Length 270;
Best Local Similarity 76.9%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EKPFEAYKAAA 13
   ||||| |||||
Db 54 EKPKEPRKAAA 66

RESULT 8
S68365
(+) -delta-cadinene synthase isozyme XC1 - Gossypium arboreum
C:Species: Gossypium arboreum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68365
R:Chen, X.Y.; Chen, Y.; Weinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A:Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A:Reference number: S68365; MUID:96132653; PMID:8554317
A:Accession: S68365
A:Molecule type: mRNA
A:Residues: 1-554 <CHE>
A:Cross-references: UNIPROT:Q39761; EMBL:U23206; NID:G1045311; PIDN:AAA93064.1; PID:G104
A:Experimental source: cultivar Nanking
C:Superfamily: vetispiradiene synthase 1
C:Keywords: phytoalexin biosynthesis

Query Match 55.3%; Score 42; DB 2; Length 554;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 KPKFEAYKAAAP 14
   ||||| :|||
Db 394 KPSFEFKNALP 406

RESULT 9
S68366
(+) -delta-cadinene synthase isozyme XC14 - Gossypium arboreum
C:Species: Gossypium arboreum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68366
R:Chen, X.Y.; Chen, Y.; Weinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A:Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A:Reference number: S68365; MUID:96132653; PMID:8554317
A:Accession: S68366
A:Molecule type: mRNA
```

```
A:Molecule type: mRNA
A:Residues: 1-554 <CHE>
A:Cross-references: UNIPROT:Q39760; EMBL:U23205; NID:G1045313; PIDN:AAA93065.1; PID:G104
A:Experimental source: cultivar Nanking
C:Superfamily: vetispiradiene synthase 1
C:Keywords: phytoalexin biosynthesis

Query Match 55.3%; Score 42; DB 2; Length 554;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 KPKFEAYKAAAP 14
   ||||| :|||
Db 394 KPSFEFKNALP 406

RESULT 10
MOCH4E
myosin alkali light chain 4, embryonic - chicken
N:Alternate names: myosin L23 catalytic light chain
C:Species: Gallus gallus (Chicken)
C:Date: 01-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: S02065; A29473
R:Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriy
J. Mol. Biol. 204, 497-505, 1988
A:Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic gi
A:Reference number: S02065; MUID:89141751; PMID:3225843
A:Accession: S02065
A:Molecule type: DNA
A:Residues: 1-185 <NAB>
A:Cross-references: UNIPROT:P09540; EMBL:X14428
A:Note: the authors translated the codon CGG for residue 71 as Ala
R:Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.
J. Biol. Chem. 262, 14408-14414, 1987
A:Title: A common myosin light chain is expressed in chicken embryonic skeletal, cardiac
A:Reference number: A29473; MUID:88032983; PMID:3667580
A:Accession: A29473
A:Molecule type: mRNA
A:Residues: 1-93, 'L', '95-165, 'L', 167-185 <KAW>
A:Cross-references: GB:J02823; NID:G212339; PIDN:AAA48957.1; PID:G212340
A:Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1
C:Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac
C:Genetics:
A:Introns: 33/3; 43/1; 93/1; 151/1; 177/1
C:Complex: The myosin molecule contains two heavy chains, two alkali light chains, and t
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: brain; calcium binding; duplication; EF hand; muscle contraction
F:39-73/Domain: calmodulin repeat homology <EF1>
F:118-150/Domain: calmodulin repeat homology <EF3>
F:153-185/Domain: calmodulin repeat homology <EF4>

Query Match 53.9%; Score 41; DB 1; Length 185;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 PKFEAYKAAAP 14
   ||| :|||
Db 8 PKDAAKAAAP 19

RESULT 11
MORT4E
myosin alkali light chain 4, embryonic and atrial - rat
N:Alternate names: MLC1A; MLC1emb; myosin L1 catalytic light chain, atrial
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jan-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: S09236
R:Romer, A.S.; McNally, E.M.; Leinwand, L.A.
Nucleic Acids Res. 18, 1581-1586, 1990
A:Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expressi
A:Reference number: S09236; MUID:90221887; PMID:2326197
A:Accession: S09236
A:Molecule type: mRNA
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A;Residues: 1-193 <R0V>  
A;Cross-references: UNIPROT:P17209; EMBL:X51531; NID:q57512; PIDN:CAA35911.1; PID:q57513  
C;Comment: In mammals, this form is found in fecal and regenerating skeletal muscle, fed  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract  
F;47-81/Domain: calmodulin repeat homology <EF1>  
F;126-158/Domain: calmodulin repeat homology <EF3>  
F;161-193/Domain: calmodulin repeat homology <EF4>

Query Match 53.9%; Score 41; DB 1; Length 193;  
Best Local Similarity 64.3%; Pred. No. 13;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPKFEAYKAAAPA 15  
Db 7 EPKKEAYKAAAPA 20

RESULT 12  
T14644  
1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO2 - sorghum (fragment)  
N;Alternate names: ACC oxidase  
C;Species: Sorghum bicolor (sorghum)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T14644  
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.  
Plant Physiol. 119, 1083-1089, 1999  
A;Title: The mechanism of rhythmic ethylene production in sorghum. The role of phytochrome  
A;Reference number: Z18166; MUID:99169299; PMID:10069847  
A;Accession: T14644  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-194 <FIN>  
A;Cross-references: UNIPROT:O81607; EMBL:AF079589; NID:g3386566; PIDN:AAC28489.1; PID:g3386566  
C;Genetics:  
A;Gene: ACO2  
C;Function:  
A;Description: involved in ethylene biosynthesis  
A;Pathway: ethylene biosynthesis  
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase  
C;Keywords: ethylene biosynthesis; oxidoreductase

Query Match 53.9%; Score 41; DB 2; Length 194;  
Best Local Similarity 53.3%; Pred. No. 13;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 15  
Db 180 KEPRFEAMKSAIATA 194

RESULT 13  
T48130  
hypothetical protein T4C9.40 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48130  
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Meyer  
submitted to the Protein Sequence Database, June 1999  
A;Reference number: Z24485  
A;Accession: T48130  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-200 <BEV>  
A;Cross-references: UNIPROT:Q9STJ1; EMBL:AL080318  
A;Experimental source: cultivar Columbia; BAC clone T4C9  
C;Genetics:  
A;Map position: 4  
A;Introns: 132/1  
A;Note: T4C9.40

Query Match 53.9%; Score 41; DB 2; Length 200;  
Best Local Similarity 69.2%; Pred. No. 14;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 13  
Db 180 EKPKEAYKAAQA 192

RESULT 14  
AG3508  
transporter BMEI2053 [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AG3508  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AG3508  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-216 <KUR>  
A;Cross-references: UNIPROT:Q8YE25; GB:AE008917; PIDN:AAL53234.1; PID:g17984111; GSPDB:G17984111  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BMEI2053  
A;Map position: 1

Query Match 53.9%; Score 41; DB 2; Length 216;  
Best Local Similarity 52.6%; Pred. No. 15;  
Matches 10; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 1 EKPKEAYKAA----AAPA 15  
Db 18 EKPFPDYASARSSDAAPA 36

RESULT 15  
T21061  
hypothetical protein F17C11.9 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T21061  
R;McMurray, A.  
submitted to the EMBL Data Library, May 1996  
A;Reference number: Z19366  
A;Accession: T21061  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-398 <WIL>  
A;Cross-references: UNIPROT:P54412; EMBL:Z72507; PIDN:CAA96631.1; GSPDB:GN00023; CESP:F17C11  
A;Experimental source: clone F17C11  
C;Genetics:  
A;Gene: CESP:F17C11.9  
A;Map position: 5  
A;Introns: 3/3; 44/3; 151/3; 196/1; 354/3  
C;Superfamily: translation elongation factor eEF-1 gamma chain

Query Match 53.9%; Score 41; DB 2; Length 398;  
Best Local Similarity 76.9%; Pred. No. 27;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 13  
Db 214 EKPKEAYKAAAPA 226

Search completed: March 31, 2005, 02:42:29  
Job time : 18.9032 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds  
(without alignments)  
95.342 Million cell updates/sec

Title: US-10-056-583A-91

Perfect score: 76

Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	69.7	781	2 Q65JG3	Q65JG3 bacillus li
2	46	60.5	299	1 RL22 DROME	P50887 drosophila
3	46	60.5	312	2 Q9UAN1	Q9uan1 drosophila
4	46	60.5	458	2 Q7SDS7	Q7sds7 neurospora
5	45	59.2	800	2 Q7UTK6	Q7utk6 rhodospirillum rubrum
6	45	59.2	1340	2 Q69YQ8	Q69yq8 homo sapien
7	45	59.2	1614	2 Q69YQ9	Q69yq9 homo sapien
8	44	57.9	192	1 MLEF MOUSE	P9326 mus musculu
9	44	57.9	315	2 P93326	P93326 musa acumin
10	44	57.9	377	2 Q7VZX6	Q7vzx6 bordetella
11	44	57.9	377	2 Q7WLP2	Q7wlp2 bordetella
12	44	57.9	377	2 Q7WQL8	Q7wql8 bordetella
13	43	56.6	306	2 Q92TW2	Q92tw2 rhizobium m
14	43	56.6	336	1 SYW NEIMA	Q91tq0 neisseria m
15	43	56.6	336	1 SYW NEIMB	Q91vq9 neisseria m
16	43	56.6	389	2 Q9AAC8	Q9aac8 caulobacter
17	43	56.6	555	2 Q7NVT5	Q7nvt5 chromobacte
18	43	56.6	574	2 Q8XMB8	Q8xmb8 drosophila
19	43	56.6	607	2 Q9W327	Q9w327 drosophila
20	43	56.6	1178	2 Q89P82	Q89p82 bradyrhizob
21	42.5	55.9	316	2 Q81606	Q81606 sorghum bic
22	42	55.3	163	2 Q6JRS4	Q6jrs4 equus caball
23	42	55.3	238	1 S8B SHEON	Q8ea81 shewanella
24	42	55.3	270	2 Q85933	Q85933 sphingomona
25	42	55.3	342	2 Q62L76	Q62l76 burkholderi
26	42	55.3	342	2 Q63V82	Q63v82 burkholderi
27	42	55.3	354	1 DPO4 PSEPK	Q88nk4 pseudomonas
28	42	55.3	508	2 Q9SW77	Q9sw77 gossypium a
29	42	55.3	551	2 Q9LKN1	Q9lkn1 gossypium h
30	42	55.3	554	1 DCS1 GOSAR	Q39761 gossypium a
31	42	55.3	554	1 DCS1_GOSHI	P93665 gossypium h

32 42 55.3 554 1 DCS2 GOSAR Q39760 gossypium a  
33 42 55.3 554 1 DCS4 GOSAR Q49853 gossypium a  
34 42 55.3 1304 2 Q6BUQ2 Q6buq2 debaryomyce  
35 41 53.9 136 2 Q8FR15 Q8fr15 corynebacte  
36 41 53.9 143 2 Q8KG95 Q8kg95 chlorobium  
37 41 53.9 185 1 MLEX CHICK P09540 gallus gall  
38 41 53.9 192 1 MLEF RAT P17209 rattus norv  
39 41 53.9 194 2 Q81607 Q81607 sorghum bic  
40 41 53.9 200 2 Q9STJ1 Q9stj1 arabidopsis  
41 41 53.9 216 2 Q8YE25 Q8ye25 bruceella me  
42 41 53.9 235 2 Q8FY17 Q8fy17 bruceella su  
43 41 53.9 249 2 Q892F2 Q892f2 clostridium  
44 41 53.9 317 2 Q6JNS3 Q6jns3 zea mays (m  
45 41 53.9 373 2 Q814K9 Q814k9 caenorhabdi

#### ALIGNMENTS

RESULT 1  
Q65JG3 PRELIMINARY; PRT; 781 AA.  
AC Q65JG3;  
DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DE SPOIIE (DNA translocase).  
GN Name=spoiie; ORFNames=BL01204, BL01906;  
OS Bacillus licheniformis DSM 13;  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=279010;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 13;  
RX PubMed=15383718;  
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,  
RA Ehrenreich A., Gottschalk G.;  
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an  
Organism with Great Industrial Potential."  
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 14580;  
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,  
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,  
RA Rasmussen M.D., Andersen J.T., Jorgensen P.B., Larsen T.S.,  
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,  
RA Berka R.M.;  
RT "Complete genome sequence of the industrial bacterium Bacillus  
licheniformis and comparisons with closely related Bacillus species."  
RL Genome Biol. 5:R77-R77(2004).  
DR EMBL; AE017333; AAU40801.1; -.  
DR EMBL; CP000002; AAU23441.1; -.  
SQ SEQUENCE 781 AA; 86477 MW; 6349A5AC2DA5D3D8 CRC64;

Query Match 69.7%; Score 53; DB 2; Length 781;  
Best Local Similarity 66.7%; Pred. No. 2.6; Mismatches 2; Indels 0; Gaps 0;  
Matches 10; Conservative 3;

Qy 1 EKPKEAYKAAAPA 15  
Db 264 EKPEQAYEAPAPA 278

RESULT 2  
RL22 DROME STANDARD; PRT; 299 AA.  
ID RL22 DROME  
AC P50887; Q9V3X9;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE 60S ribosomal protein L22.



GN Name=RpL22; ORFNames=CG7434;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
RP "From sequence to chromosome: the tip of the X chromosome of D.  
RP melanogaster".  
RL Glover C.V.C., Bidwai A.P., Zhao W.F.;  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
[2]  
RN  
RC STRAIN=Berkley;  
RC MEDLINE=20196006; PubMed=10731137; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.P.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abiril J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,  
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foder C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster".  
RL Science 287:2185-2195 (2000).  
[3]  
RP GENOME REANNOTATION  
RP MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.B.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review".  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).  
[4]  
RN  
RC STRAIN=Oregon-R;  
RC MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;  
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
RA Barrall B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,  
RA Dreano S., Gloux S., Lelaire V., Mottier S., Galibert F., Borkova D.,  
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,  
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,  
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,  
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,  
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
RA Glover D.M.;  
RT "From sequence to chromosome: the tip of the X chromosome of D.  
RT melanogaster".  
RL Science 287:2220-2222 (2000).  
CC -1- SIMILARITY: Belongs to the ribosomal protein L22e family.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: U42587; AAB17433.1; --  
CC EMBL: AE003418; AAF45546.1; --  
CC EMBL: AL132792; CAB60023.1; --  
CC IntAct; P50887; --  
CC FlyBase; FBgn0015288; RPL22.  
CC InterPro; IPR002671; Ribosomal L22e.  
CC Pfam; PF01776; Ribosomal L22e; 1  
CC ProDom; PD007306; Ribosomal\_L22e; 1.  
KW Ribosomal protein.  
FT DOMAIN 24 31 Poly-Ala.  
FT DOMAIN 46 50 Poly-Ala.  
FT DOMAIN 65 70 Poly-Ala.  
FT DOMAIN 93 98 Poly-Ala.  
FT DOMAIN 103 112 Poly-Ala.  
FT DOMAIN 136 152 Poly-Ala.  
FT DOMAIN 185 188 Poly-Lys.  
FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).  
SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;  
  
Query Match 60.5%; Score 46; DB 1; Length 299;  
Best Local Similarity 73.3%; Pred. No. 17;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ERKPFEEAYKAAAPA 15  
Db |||||  
36 ERKFAEAKPAAAAA 50  
  
RESULT 3  
Q9UAN1 PRELIMINARY; PRT; 312 AA.  
AC Q9UAN1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein L22 (Fragment).  
GN Name=RpL22; Synonyms=rpl22;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99132306; PubMed=9911508; DOI=10.1016/S0378-1119(98)00529-0;  
RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;  
RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal  
RT proteins, L22 and L23a, with unique histone-like amino-terminal  
RT extensions.";  
RL Gene 226:339-345 (1999).  
DR EMBL; AF080131; AAD19341.1; --  
DR FlyBase; FBgn0015288; RPL22.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.



```
DR GO: GO:0003735; F: structural constituent of ribosome; IEA.
DR GO: GO:0006412; P: protein biosynthesis; IEA.
DR InterPro: IPR002671; Ribosomal_L22e.
DR Pfam: PF01776; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 312 AA; 32273 MW; 0B59A15CB473083B CRC64;

Query Match 60.5%; Score 46; DB 2; Length 312;
Best Local Similarity 73.3%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAP 15
Db 49 EKPKAEAAKPAAPAAA 63

RESULT 4
Q7SDS7 PRELIMINARY; PRT; 458 AA.
ID Q7SDS7
AC Q7SDS7;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben E.L., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kanal M., Kamysov S., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000044; EAA34940.1; -
SQ SEQUENCE 458 AA; 49949 MW; 196D609BF9320496 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 458;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAP 15
Db 78 QKPKQAKAKAPAA 92

RESULT 5
Q7UTK6 PRELIMINARY; PRT; 800 AA.
ID Q7UTK6
AC Q7UTK6;
RA 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB3828;

OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=1117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL: BX294139; CAD73430.1; -
DR InterPro: IPR001345; PG/BCPM_mutase.
DR PROSITE: PS00175; PG_MUTASE; UNKNOWN 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 800 AA; 91385 MW; C32C861687CDB466 CRC64;

Query Match 59.2%; Score 45; DB 2; Length 800;
Best Local Similarity 57.1%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KPKEAYKAAAP 15
Db 773 KPANDAYKSIATPA 786

RESULT 6
Q69YQ8 PRELIMINARY; PRT; 1340 AA.
ID Q69YQ8
AC Q69YQ8;
RA 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp451i127 (Fragment).
GN Name=DKFZp451i127;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RG The German cDNA Consortium;
RA Koshner K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL832376; CAH10402.1; -
KW Hypothetical protein.
FT NON TER 1340 1340
SQ SEQUENCE 1340 AA; 145772 MW; FA4635B5BE64394 CRC64;

Query Match 59.2%; Score 45; DB 2; Length 1340;
Best Local Similarity 64.3%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAP 14
Db 634 ENEEFAYSPAAAP 647

RESULT 7
Q69YQ9 PRELIMINARY; PRT; 1614 AA.
ID Q69YQ9
AC Q69YQ9;
RA 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp451A076 (Fragment).
GN Name=DKFZp451A076;
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Skeletal muscle;  
 RA The German cDNA Consortium;  
 RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S., to the EMBL/GenBank/DBJ databases.  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL832347; CAH10406.1; -  
 KW Hypothetical protein.  
 FT NON TER 1614 1614  
 SQ SEQUENCE 1614 AA; 175041 MW; FCE219C927BAEB9B CRC64;  
 Query Match 59.2%; Score 45; DB 2; Length 1614;  
 Best Local Similarity 64.3%; Pred. No. 1.2e+02;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EKPKFEAYKAAAP 14  
 Db :||| |||||  
 562 ENEEFAYSPAAP 575  
 RESULT 8  
 MLEF MOUSE STANDARD; PRT; 192 AA.  
 AC P09541;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Myosin light chain 1, atrial/fetal isoform (MLC1A) (MLCIEMB).  
 GN Name=Mc1a; Synonyms=My1a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=C3H;  
 RX MEDLINE=88315068; PubMed=2842339;  
 RA Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,  
 RA Buckingham M.E.;  
 RT "Structure and sequence of the myosin alkali light chain gene  
 expressed in adult cardiac atria and fetal striated muscle.";  
 RL J. Biol. Chem. 263:12669-12676(1988).  
 RN [2]  
 RP SEQUENCE OF 1-40 FROM N.A.  
 RC STRAIN=C3H;  
 RX MEDLINE=89057447; PubMed=3194193;  
 RA Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,  
 RA Buckingham M.E.;  
 RT "Promoter analysis of myosin alkali light chain genes expressed in  
 mouse striated muscle.";  
 RL Nucleic Acids Res. 16:10037-10052(1988).  
 CC -1- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light  
 chains.  
 CC -1- TISSUE SPECIFICITY: Expressed in atrial muscle and in fetal  
 skeletal and ventricular muscle.  
 CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS  
 PROTEIN DOES NOT BIND CALCIUM.  
 CC -----  
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 CC -----  
 DR EMBL; M20772; AAA39721.1; -  
 DR EMBL; M31017; AAA39721.1; JOINED.  
 DR EMBL; M20769; AAA39721.1; JOINED.

DR EMBL; M20770; AAA39721.1; JOINED.  
 DR EMBL; M20771; AAA39721.1; JOINED.  
 DR EMBL; X12971; CAA31414.1; -  
 DR EMBL; M19436; AAA39720.1; -  
 DR PIR; A31114; MOWS4E.  
 DR HSP; P02607; 1BR1.  
 DR MGD; MGI:97267; Myla.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF-hand like.  
 DR ProDom; PD000012; EF-hand; 2.  
 KW Multigene family; Muscle protein; Myosin.  
 FT INIT MET 0  
 SQ SEQUENCE 192 AA; 21028 MW; B0439D512FA19C38 CRC64;  
 Query Match 57.9%; Score 44; DB 1; Length 192;  
 Best Local Similarity 71.4%; Pred. No. 24;  
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 KPKEAYKAAAP 15  
 Db :||| |||||  
 6 EPKEAAKPAAP 19  
 RESULT 9  
 P93326 PRELIMINARY; PRT; 315 AA.  
 ID P93326;  
 AC P93326;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 1-aminocyclopropane-1-carboxylate oxidase.  
 GN Name=baol;  
 OS Musa acuminata (Banana).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;  
 OC Musa.  
 OX NCBI\_TaxID=4641;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP TISSUE=Fruit;  
 RA Liu J.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the iron/ascorbate-dependent oxidoreductase  
 family.  
 CC EMBL; X95599; CAA64856.1; -  
 DR HSP; Q96323; IGP6.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR005123; 2OG-FeII\_Oxy.  
 DR Pfam; PF03171; 2OG-FeII\_Oxy; 1.  
 KW Iron; Oxidoreductase  
 SQ SEQUENCE 315 AA; 35348 MW; 9EA22912E6F0BE43 CRC64;  
 Query Match 57.9%; Score 44; DB 2; Length 315;  
 Best Local Similarity 57.1%; Pred. No. 38;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 EKPKFEAYKAAAP 14  
 Db :||| |||||  
 298 KEPRFAMKATAP 311  
 RESULT 10  
 Q7VZX6 PRELIMINARY; PRT; 377 AA.  
 ID Q7VZX6;  
 AC Q7VZX6;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Probable GTP-binding protein.  
 GN OrderedLocNames=BP0747;  
 OS Bordetella pertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.



```

OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngi1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640413; CAE41053.1; -.
DR HSSP; P44681; IJAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.
DR InterPro; IPR006169; GTP1_OBG_sub.
DR InterPro; IPR002917; MMR_HSR1.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKPKEAYKAAAPAA 15
Db 356 EDPRFASRGGAAPA 370

RESULT 11
Q7W1P2 PRELIMINARY; PRT; 377 AA.
AC Q7W1P2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable GTP-binding protein.
GN OrderedLocustNames=BPP0309;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngi1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640423; CAE40050.1; -.
DR HSSP; P44681; IJAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.

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DR InterPro; IPR006169; GTP1_OBG_sub.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKPKEAYKAAAPAA 15
Db 356 EDPRFASRGGAAPA 370

RESULT 12
Q7WQL8 PRELIMINARY; PRT; 377 AA.
AC Q7WQL8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable GTP-binding protein.
GN OrderedLocustNames=BB0312;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngi1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640437; CAE30810.1; -.
DR HSSP; P44681; IJAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.
DR InterPro; IPR006169; GTP1_OBG_sub.
DR InterPro; IPR002917; MMR_HSR1.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EKPKEAYKAAAPAA 15
Db 356 EDPRFASRGGAAPA 370

RESULT 13
Q92TW2 PRELIMINARY; PRT; 306 AA.
ID Q92TW2
AC Q92TW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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 DR EMBL; AE002496; AAF41828.1; -;  
 DR PIR; B81081; B81081.  
 DR HSP; P00953; 1MAU.  
 DR TIGR; NMB1471; -;  
 DR HAMAP; MF\_00140; -; 1.  
 DR InterPro; IPR002305; trna-synt\_1b.  
 DR InterPro; IPR001412; trna-synt\_1.  
 DR InterPro; IPR002306; TTP trna-synt\_1b.  
 DR Pfam; PF00579; trna-synt\_1b; 1.  
 DR PRINTS; PRO1039; TRNASYNTHTRP.  
 DR PROSITE; PS00178; AA TRNA\_LIGASE\_I; FALSE NEG.  
 KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;  
 KW Protein biosynthesis.  
 FT SITE 12 20 "HIGH" region.  
 FT SITE 203 207 "KMSKS" region.  
 FT BINDING 206 206 ATP (by similarity).  
 SQ SEQUENCE 336 AA; 37616 MW; 0AE32C8C00B621AA CRC64;

Query Match 56.6%; Score 43; DB 1; Length 336;  
 Best Local Similarity 53.3%; Pred. No. 60;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 15  
 | | | | | : | :  
 Db 243 ESPLFEIYKAPSTPS 257

Search completed: March 31, 2005, 02:41:11  
 Job time : 82.5645 secs



**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds  
(without alignments)  
65.338 Million cell updates/sec

Title: US-10-056-583A-95

Perfect score: 69

Sequence: 1 EKAFKFAKAAAAA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	15	5	Abp52301 HLA-DR2 m
2	64	92.8	17	5	Abp52302 HLA-DR2 m
3	63	91.3	15	5	Abp52271 HLA-DR2 m
4	63	91.3	15	5	Abp52298 HLA-DR2 m
5	63	91.3	17	5	Abp52294 HLA-DR2 m
6	63	91.3	17	5	Abp52296 HLA-DR2 m
7	63	91.3	19	5	Abp52295 HLA-DR2 m
8	61	88.4	17	5	Abp52303 HLA-DR2 m
9	57	82.6	15	5	Abp52270 HLA-DR2 m
10	56	81.2	15	5	Abp52297 HLA-DR2 m
11	53	76.8	15	5	Abp52291 HLA-DR2 m
12	53	76.8	15	5	Abp52263 HLA-DR2 m
13	52	75.4	15	5	Abp52272 HLA-DR2 m
14	51	73.9	15	5	Abp52259 HLA-DR2 m
15	51	73.9	15	5	Abp52257 HLA-DR2 m
16	50	72.5	15	5	Abp52300 HLA-DR2 m
17	50	72.5	15	5	Abp52304 HLA-DR2 m
18	49	71.0	15	5	Abp52299 HLA-DR2 m
19	48	69.6	15	5	Abp52253 HLA-DR2 m
20	48	69.6	15	5	Abp52251 HLA-DR2 m
21	48	69.6	15	5	Abp52239 HLA-DR2 m
22	47	68.1	15	5	Abp52290 HLA-DR2 m
23	47	68.1	15	5	Abp52261 HLA-DR2 m
24	47	68.1	15	5	Abp52244 HLA-DR2 m
25	47	68.1	15	5	Abp52292 HLA-DR2 m

26	47	68.1	15	5	Abp52269 HLA-DR2 m
27	47	68.1	15	5	Abp52262 HLA-DR2 m
28	46	66.7	15	5	Abp52264 HLA-DR2 m
29	46	66.7	15	5	Abp52267 HLA-DR2 m
30	46	66.7	15	5	Abp52236 HLA-DR2 m
31	44	63.8	15	5	Abp52265 HLA-DR2 m
32	44	63.8	15	5	Abp52277 HLA-DR2 m
33	44	63.8	15	5	Abp52280 HLA-DR2 m
34	43	62.3	15	5	Abp52254 HLA-DR2 m
35	43	62.3	15	5	Abp52255 HLA-DR2 m
36	43	62.3	15	5	Abp52240 HLA-DR2 m
37	43	62.3	15	5	Abp52241 HLA-DR2 m
38	43	62.3	15	5	Abp52248 HLA-DR2 m
39	43	62.3	15	5	Abp52249 HLA-DR2 m
40	43	62.3	15	5	Abp52305 HLA-DR2 m
41	43	62.3	299	4	Abp63276 Drosophil
42	43	62.3	299	8	AdS96704
43	42	60.9	15	3	AAy58969 Copeptide
44	42	60.9	15	3	AAy82058 MHC class
45	42	60.9	15	4	AAg63198 Peptide w

ALIGNMENTS

RESULT 1

ABP52301

ID ABP52301 standard; peptide; 15 AA.

XX AC ABP52301;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:95.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; anti-inflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX DR WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major  
histocompatibility complex class II HLA-DR2 protein, useful for treating a  
demyelinating disease, e.g. multiple sclerosis, or post-viral  
encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide  
with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
residues. The complex of the peptide with a major histocompatibility  
complex (MHC) class II HLA-DR2 protein is involved in modulating an  
immune response. (I) has antiinflammatory and neuroprotective activities,  
and can be used as a MHC class II protein inhibitor. The compositions  
comprising the peptides are useful for treating demyelinating diseases



CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 69; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EKAKFEAFKAAAAA 15  
 DB 1 EKAKFEAFKAAAAA 15  
 RESULT 2  
 ID ABP52302 standard; peptide; 17 AA.  
 AC ABP52302;  
 DT 16-OCT-2002 (first entry)  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:96.  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 DR WPI; 2002-608439/65.  
 XX  
 CC New compositions comprising synthetic peptides in complex with a major  
 CC histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 CC demyelinating disease, e.g. multiple sclerosis, or post-viral  
 CC encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention

SQ Sequence 17 AA;  
 Query Match 92.8%; Score 64; DB 5; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 0.00087;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EKAKFEAFKAAAAA 15  
 DB 3 EKAKFEAFKAAAAA 17  
 RESULT 3  
 ID ABP52271 standard; peptide; 15 AA.  
 XX ABP52271;  
 AC ABP52271;  
 XX  
 DT 16-OCT-2002 (first entry)  
 DE HLA-DR2 molecule binding peptide SEQ ID NO:65.  
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
 KW immune response; antiinflammatory; neuroprotective; proliferation;  
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
 KW anti-tumour necrosis factor agent.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200259143-A2.  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US002071.  
 XX  
 PR 24-JAN-2001; 2001US-0263569P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Strominger JL, Fridkis-Hareli M;  
 XX  
 DR WPI; 2002-608439/65.  
 XX  
 CC New compositions comprising synthetic peptides in complex with a major  
 CC histocompatibility complex class II HLA-DR2 protein, useful for treating a  
 CC demyelinating disease, e.g. multiple sclerosis, or post-viral  
 CC encephalomyelitis.  
 XX  
 PS Claim 28; Page 39; 54pp; English.  
 XX  
 CC The present invention describes compositions (I) comprising a peptide  
 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
 CC residues. The complex of the peptide with a major histocompatibility  
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
 CC immune response. (I) has antiinflammatory and neuroprotective activities,  
 CC and can be used as a MHC class II protein inhibitor. The compositions  
 CC comprising the peptides are useful for treating demyelinating diseases  
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
 CC demyelinating condition, and a side effect of administering an anti-  
 CC tumour necrosis factor agents. The peptide further inhibits proliferation  
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
 CC ABP52305 represent peptides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 91.3%; Score 63; DB 5; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.0011;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EKAKFEAFKAAAAA 15







KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200259143-A2.  
PN  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
PS  
XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 91.3%; Score 63; DB 5; Length 17;  
Best Local Similarity 86.7%; Pred. No. 0.0013;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EKAKFEAFKAAAAA 15  
Dy 1 EKAKYEAYKAAAAA 15  
RESULT 7  
ABP52295  
ID ABP52295 standard; peptide; 19 AA.  
XX  
XX ABP52295;  
AC  
XX 16-OCT-2002 (first entry)  
DT  
XX HLA-DR2 molecule binding peptide SEQ ID NO:89.  
DE  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
PN  
XX 01-AUG-2002.  
PD  
XX  
XX 24-JAN-2002; 2002WO-US002071.  
PF  
XX  
XX 24-JAN-2001; 2001US-0263569P.  
PR  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Strominger JL, Fridkis-Hareli M;  
PI  
XX WPI; 2002-608439/65.  
DR  
XX  
XX New compositions comprising synthetic peptides in complex with a major  
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a  
PT demyelinating disease, e.g. multiple sclerosis, or post-viral  
PT encephalomyelitis.  
XX  
XX Claim 28; Page 39; 54pp; English.  
PS  
XX The present invention describes compositions (I) comprising a peptide  
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine  
CC residues. The complex of the peptide with a major histocompatibility  
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an  
CC immune response. (I) has antiinflammatory and neuroprotective activities,  
CC and can be used as a MHC class II protein inhibitor. The compositions  
CC comprising the peptides are useful for treating demyelinating diseases  
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine  
CC demyelinating condition, and a side effect of administering an anti-  
CC tumour necrosis factor agents. The peptide further inhibits proliferation  
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to  
CC ABP52305 represent peptides used in the exemplification of the present  
CC invention  
XX  
XX Sequence 19 AA;  
SQ  
Query Match 91.3%; Score 63; DB 5; Length 19;  
Best Local Similarity 86.7%; Pred. No. 0.0014;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 EKAKFEAFKAAAAA 15  
Dy 3 EKAKYEAYKAAAAA 17  
RESULT 8  
ABP52303  
ID ABP52303 standard; peptide; 17 AA.  
XX  
XX ABP52303;  
AC  
XX 16-OCT-2002 (first entry)  
DT  
XX HLA-DR2 molecule binding peptide SEQ ID NO:97.  
DE  
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;  
KW immune response; antiinflammatory; neuroprotective; proliferation;  
KW MHC class II protein inhibitor; demyelinating disease; inhibition;  
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;  
KW anti-tumour necrosis factor agent.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX WO200259143-A2.  
PN  
XX 01-AUG-2002.  
PD  
XX



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PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 17 AA;
SQ
Query Match 88.4%; Score 61; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0027;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAAAA 15
| | | | | : | | | | |
Db 3 EKAKFEAYKAAAAA 17
| | | | | : | | | | |

RESULT 9
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
XX
AC ABP52270;
XX
XX 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX immune response; antiinflammatory; neuroprotective; proliferation;
XX MHC class II protein inhibitor; demyelinating disease; inhibition;
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
XX Sequence 15 AA;
SQ
Query Match 82.6%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAAAA 15
| | | | | : | | | | |
Db 1 EAAKFEAYKAAAAA 15
| | | | | : | | | | |

RESULT 10
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
XX
AC ABP52297;
XX
XX 16-OCT-2002 (first entry)
XX
XX HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
XX immune response; antiinflammatory; neuroprotective; proliferation;
XX MHC class II protein inhibitor; demyelinating disease; inhibition;
XX post-viral encephalomyelitis; post-vaccine demyelinating condition;
XX anti-tumour necrosis factor agent.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200259143-A2.
XX
XX 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

```



XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide

XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

XX CC residues. The complex of the peptide with a major histocompatibility

XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

XX CC immune response. (I) has antiinflammatory and neuroprotective activities

XX CC and can be used as a MHC class II protein inhibitor. The compositions

XX CC comprising the peptides are useful for treating demyelinating diseases

XX CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

XX CC demyelinating condition, and a side effect of administering an anti-

XX CC tumour necrosis factor agents. The peptide further inhibits proliferation

XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

XX CC ABP52305 represent peptides used in the exemplification of the present

XX CC invention

XX SQ Sequence 15 AA;

Query Match 81.2%; Score 56; DB 5; Length 15;

Best Local Similarity 80.0%; Pred. NO. 0.016;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15

DB 1 EKPKFEAYKAAAAA 15

RESULT 11

ABP52291

ID ABP52291 standard; peptide; 15 AA.

XX AC ABP52291;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:85.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX KW immune response; antiinflammatory; neuroprotective; proliferation;

XX KW MHC class II protein inhibitor; demyelinating disease; inhibition;

XX KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX PS WPI; 2002-608439/65.

XX CC New compositions comprising synthetic peptides in complex with a major

XX CC histocompatibility complex class II HLA-DR2 protein, useful for treating a

XX CC demyelinating disease, e.g. multiple sclerosis, or post-viral

XX CC encephalomyelitis.

XX CC Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide

XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

XX CC residues. The complex of the peptide with a major histocompatibility

XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX SQ Sequence 15 AA;

Query Match 76.8%; Score 53; DB 5; Length 15;

Best Local Similarity 73.3%; Pred. NO. 0.049;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15

DB 1 EKPKFEAYKAAAAA 15

RESULT 12

ABP52263

ID ABP52263 standard; peptide; 15 AA.

XX AC ABP52263;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:57.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX KW immune response; antiinflammatory; neuroprotective; proliferation;

XX KW MHC class II protein inhibitor; demyelinating disease; inhibition;

XX KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX PS WPI; 2002-608439/65.

XX CC New compositions comprising synthetic peptides in complex with a major

XX CC histocompatibility complex class II HLA-DR2 protein, useful for treating a

XX CC demyelinating disease, e.g. multiple sclerosis, or post-viral

XX CC encephalomyelitis.

XX CC Example 1; Page 33; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide

XX CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

XX CC residues. The complex of the peptide with a major histocompatibility

XX CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

XX CC immune response. (I) has antiinflammatory and neuroprotective activities,

XX CC and can be used as a MHC class II protein inhibitor. The compositions

XX CC comprising the peptides are useful for treating demyelinating diseases

XX CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

XX CC demyelinating condition, and a side effect of administering an anti-

XX CC tumour necrosis factor agents. The peptide further inhibits proliferation

XX CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to



Matches	11;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0
QY	1	EKAKEFAFKAAAAAA	15						
		:   :   :   :   :							
Db	1	EAKKYEAYKAAAAAA	15						
RESULT 14									
ABP52259									
ID	ABP52259	standard;	peptide;	15	AA.				
XX	AC	ABP52259;							
XX	XX	16-OCT-2002	(first entry)						
XX	XX	HLA-DR2	molecule binding peptide	SEQ	ID	NO:	53.		
XX	DE	Human leukocyte antigen; HLA; major histocompatibility complex; MHC;							
XX	KW	HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;							
XX	KW	immune response; anti-inflammatory; neuroprotective; proliferation;							
XX	KW	MHC class II protein inhibitor; demyelinating disease; inhibition;							
XX	KW	post-viral encephalomyelitis; post-vaccine demyelinating condition;							
XX	KW	anti-tumour necrosis factor agent.							
XX	OS	Homo sapiens.							
XX	OS	Synthetic.							
XX	PN	WO200259143-A2.							
XX	XX	01-AUG-2002.							
XX	PF	24-JAN-2002; 2002WO-US002071.							
XX	PR	24-JAN-2001; 2001US-0263569P.							
XX	PA	(HARD ) HARVARD COLLEGE.							
XX	PI	Strominger JL, Fridkis-Hareli M;							
XX	DR	WPI; 2002-608439/65.							
XX	PT	New compositions comprising synthetic peptides in complex with a major							
XX	PT	histocompatibility complex class II HLA-DR2 protein, useful for treating a							
XX	PT	demyelinating disease, e.g. multiple sclerosis, or post-viral							
XX	PT	encephalomyelitis.							
XX	PS	Example 1; Page 33; 54pp; English.							
XX	CC	The present invention describes compositions (I) comprising a peptide							
XX	CC	with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine							
XX	CC	residues. The complex of the peptide with a major histocompatibility							
XX	CC	complex (MHC) class II HLA-DR2 protein is involved in modulating an							
XX	CC	immune response. (I) has antiinflammatory and neuroprotective activities,							
XX	CC	and can be used as a MHC class II protein inhibitor. The compositions							
XX	CC	comprising the peptides are useful for treating demyelinating diseases							
XX	CC	such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine							
XX	CC	demyelinating condition, and a side effect of administering an anti-							
XX	CC	tumour necrosis factor agents. The peptide further inhibits proliferation							
XX	CC	of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to							
XX	CC	ABP52305 represent peptides used in the exemplification of the present							
XX	CC	invention							
XX	SQ	Sequence 15 AA;							
Query Match 73.9%; Score 51; DB 5; Length 15;									
Best Local Similarity 73.3%; Pred. No. 0.11;									
Matches	11;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0
QY	1	EKAKEFAFKAAAAAA	15						
		:   :   :   :   :							
Db	1	EKAAYAYKAAAAAA	15						



```

RESULT 15
ABP52257
ID ABP52257 standard; peptide; 15 AA.
XX
AC ABP52257;
XX
DT 16-OCT-2002 (first entry)
XX
HLA-DR2 molecule binding peptide SEQ ID NO:51.
XX
Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
FI Strominger JL, Fridkis-Harell M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 32; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
XX
Query Match 73.9%; Score 51; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.11;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAAAA 15
Db 1 EAAKYAAYKAAAAA 15

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Search completed: March 31, 2005, 02:35:28  
Job time : 88.7903 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds  
(without alignments)  
48.718 Million cell updates/sec

Title: US-10-056-583A-95

Perfect score: 69  
Sequence: 1 EKXFEAFKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/ECTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	58.0	1001	4	US-09-248-796A-18658
2	39	56.5	166	4	US-09-252-991A-22139
3	39	56.5	466	4	US-09-489-039A-13950
4	38	55.1	13	5	PCT-US95-04121-38
5	38	55.1	497	1	US-08-295-670-6
6	38	55.1	497	1	US-08-633-485-6
7	38	55.1	510	3	US-08-508-761B-4
8	37	53.6	38	3	US-09-117-121-16
9	37	53.6	38	3	US-09-117-121-24
10	37	53.6	38	4	US-09-344-529-5
11	37	53.6	69	4	US-09-248-796A-25516
12	37	53.6	476	4	US-09-198-452A-1021
13	37	53.6	479	4	US-09-438-185A-950
14	37	53.6	576	4	US-09-543-681A-7747
15	37	53.6	759	4	US-09-328-352-4241
16	36	52.2	13	5	PCT-US94-10257A-33
17	36	52.2	54	3	US-09-117-121-30
18	36	52.2	162	4	US-09-732-210-1445
19	36	52.2	180	6	5273901-7
20	36	52.2	180	6	5482709-6
21	36	52.2	180	6	5273901-7
22	36	52.2	180	6	5482709-6
23	36	52.2	405	4	US-09-328-352-4239
24	36	52.2	582	4	US-09-919-497-100
25	35	50.7	10	4	US-09-060-450-5
26	35	50.7	109	4	US-09-405-743A-7
27	35	50.7	109	4	US-09-816-989A-7

ALIGNMENTS

RESULT 1

US-09-248-796A-18658  
; Sequence 18658, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18658  
; LENGTH: 1001  
; TYPE: PRT  
; ORGANISM: Candida albicans  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (21)  
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown  
US-09-248-796A-18658

Query Match 58.0%; Score 40; DB 4; Length 1001;  
Best Local Similarity 78.6%; Pred. No. 1.6e+02;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAKFEAFKAAAAA 15  
||| || |||||  
DB 818 KAKEAEAAAAAAA 831

RESULT 2

US-09-252-991A-22139  
; Sequence 22139, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27



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; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
PCT-US95-04121-38

Query Match          55.1%; Score 38; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 4.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 AKFEAFKAAAAA 15
       |.:| |||||
Db      1 AAYKAAKAAAAA 13

RESULT 5
US-08-295-670-6
; Sequence 6, Application US/08295670
; Patent No. 5547864
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: MIWA, KIYOSHI
; APPLICANT: KAWAHARA, YOSHIO
;
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,670
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00039
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-4069
; FILING DATE: 13-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5547864man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-697-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-295-670-6

Query Match          55.1%; Score 38; DB 1; Length 497;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 EKAKFEAFKAAAAA 15
       |.:| |||||

```



Db 104 EQAAFEAFEAARVRA 118

RESULT 6

US-08-633-485-6

Sequence 6, Application US/08633485

Patent No. 5681717

GENERAL INFORMATION:

APPLICANT: KAWASAKI, HISASHI

APPLICANT: TSUCHIYA, NAKOTO

APPLICANT: MIWA, KIVOSHI

APPLICANT: KAWAHARA, YOSHIO

TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,485

FILING DATE: 17-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/295,670

FILING DATE: 08-SEP-1994

APPLICATION NUMBER: PCT/JP94/00039

FILING DATE: 13-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-4069

FILING DATE: 13-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5681717man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-697-0 PCT

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 497 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-633-485-6

Query Match 55.1%; Score 38; DB 1; Length 497;

Best Local Similarity 53.3%; Pred. No. 1.6e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15

Db 104 EQAAFEAFEAARVRA 118

RESULT 7

US-08-508-761B-4

Sequence 4, Application US/08508761B

Patent No. 6027920

GENERAL INFORMATION:

APPLICANT: Joliff, Gwennael

APPLICANT: Guyonvarch, Arnel

APPLICANT: Purification, Relano

APPLICANT: Duchiron, Francis

TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/117,121

FILING DATE: 20-NOV-1998

US-08-508-761B-4

Query Match 55.1%; Score 38; DB 3; Length 510;

Best Local Similarity 53.3%; Pred. No. 1.7e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15

Db 104 EQAAFEAFEAARVRA 118

RESULT 8

US-09-117-121-16

Sequence 16, Application US/09117121

Patent No. 6307020

GENERAL INFORMATION:

APPLICANT: Hew, Choy

APPLICANT: Gong, Zhiyuan

TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/117,121

FILING DATE: 20-NOV-1998

US-08-508-761B-4

Query Match 55.1%; Score 38; DB 3; Length 510;

Best Local Similarity 53.3%; Pred. No. 1.7e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15

Db 104 EQAAFEAFEAARVRA 118



```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 016252-001610US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-117-121-16

Query Match 53.6%; Score 37; DB 3; Length 38;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
DB 16 KAAAEATKAAAAA 29

RESULT 9
US-09-117-121-24
; Sequence 24, Application US/09117121
; Patent No. 6307020
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy
; APPLICANT: Gong, Zhiyuan
; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
; TITLE OF INVENTION: and Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/117,121
; FILING DATE: 20-NOV-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00062
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 016252-001610US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-117-121-24

Query Match 53.6%; Score 37; DB 3; Length 38;

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```

Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
DB 16 KAAAEATKAAAAA 29

RESULT 10
US-09-344-529-5
; Sequence 5, Application US/09344529
; Patent No. 6429293
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy L.
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
; FILE REFERENCE: 016252-002620US
; CURRENT APPLICATION NUMBER: US/09/344,529
; CURRENT FILING DATE: 1999-06-24
; EARLIER APPLICATION NUMBER: US 60/090,794
; EARLIER FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: US 60/095,713
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Pleuronectes americanus
; FEATURE:
; OTHER INFORMATION: Winter flounder skin-type antifreeze polypeptide
; OTHER INFORMATION: (wfsAPP-1)
US-09-344-529-5

Query Match 53.6%; Score 37; DB 4; Length 38;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
DB 16 KAAAEATKAAAAA 29

RESULT 11
US-09-248-796A-25516
; Sequence 25516, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25516
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25516

Query Match 53.6%; Score 37; DB 4; Length 69;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
DB 8 EAKLDTFFAAATAA 21

```



```
RESULT 12
US-09-198-452A-1021
; Sequence 1021, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1021
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1021

Query Match      53.6%; Score 37; DB 4; Length 476;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      4 KFEAFKAAAAA 14
      :| ||| |||||
Db     107 RFSAFAAAAA 117

RESULT 13
US-09-438-185A-950
; Sequence 950, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 950
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0948
US-09-438-185A-950

Query Match      53.6%; Score 37; DB 4; Length 479;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      4 KFEAFKAAAAA 14
      :| ||| |||||
Db     110 RFSAFAAAAA 120

RESULT 14
US-09-543-681A-7747
; Sequence 7747, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
```

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; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7747
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7747

Query Match      53.6%; Score 37; DB 4; Length 576;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EKAFKFAKAAAA 14
      :| :| :| :| :|
Db     311 EEEQFQAYKAAEA 324

RESULT 15
US-09-328-352-4241
; Sequence 4241, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4241
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4241

Query Match      53.6%; Score 37; DB 4; Length 759;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 KAKFEAFKAAAAA 15
      :| :| :| :| :|
Db     444 KAKEEQAKAAKAA 457

Search completed: March 31, 2005, 02:44:10
Job time : 23.9839 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds  
(without alignments)  
74.648 Million cell updates/sec

Title: US-10-056-583A-95

Perfect score: 69  
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	15	14	US-10-056-583-95
2	64	92.8	17	14	US-10-056-583-96
3	63	91.3	15	14	US-10-056-583-65
4	63	91.3	17	14	US-10-056-583-88
5	63	91.3	17	14	US-10-056-583-90
6	63	91.3	19	14	US-10-056-583-89
7	61	88.4	17	14	US-10-056-583-97
8	57	82.6	15	14	US-10-056-583-64
9	57	82.6	15	14	US-10-056-583-92
10	56	81.2	15	14	US-10-056-583-91
11	53	76.8	15	14	US-10-056-583-57
12	53	76.8	15	14	US-10-056-583-85
13	52	75.4	15	14	US-10-056-583-66

14	73.9	15	14	US-10-056-583-51	Sequence 51, Appl
15	73.9	15	14	US-10-056-583-53	Sequence 53, Appl
16	72.5	15	14	US-10-056-583-94	Sequence 94, Appl
17	72.5	15	14	US-10-056-583-98	Sequence 98, Appl
18	71.0	15	14	US-10-056-583-93	Sequence 93, Appl
19	69.6	15	14	US-10-056-583-33	Sequence 33, Appl
20	69.6	15	14	US-10-056-583-45	Sequence 45, Appl
21	69.6	15	14	US-10-056-583-47	Sequence 47, Appl
22	68.1	15	14	US-10-056-583-38	Sequence 38, Appl
23	68.1	15	14	US-10-056-583-55	Sequence 55, Appl
24	68.1	15	14	US-10-056-583-56	Sequence 56, Appl
25	68.1	15	14	US-10-056-583-63	Sequence 63, Appl
26	68.1	15	14	US-10-056-583-84	Sequence 84, Appl
27	66.7	15	14	US-10-056-583-30	Sequence 86, Appl
28	66.7	15	14	US-10-056-583-34	Sequence 30, Appl
29	66.7	15	14	US-10-056-583-58	Sequence 58, Appl
30	66.7	15	14	US-10-056-583-61	Sequence 61, Appl
31	63.8	15	14	US-10-056-583-59	Sequence 59, Appl
32	63.8	15	14	US-10-056-583-71	Sequence 71, Appl
33	63.8	15	14	US-10-056-583-74	Sequence 74, Appl
34	62.3	15	14	US-10-056-583-34	Sequence 34, Appl
35	62.3	15	14	US-10-056-583-35	Sequence 35, Appl
36	62.3	15	14	US-10-056-583-42	Sequence 42, Appl
37	62.3	15	14	US-10-056-583-43	Sequence 43, Appl
38	62.3	15	14	US-10-056-583-48	Sequence 48, Appl
39	62.3	15	14	US-10-056-583-49	Sequence 49, Appl
40	62.3	15	14	US-10-056-583-99	Sequence 99, Appl
41	62.3	99	16	US-10-437-963-141270	Sequence 141270,
42	62.3	142	16	US-10-437-963-141271	Sequence 141271,
43	60.9	15	9	US-09-765-301-24	Sequence 24, Appl
44	60.9	15	10	US-09-765-644A-24	Sequence 24, Appl
45	60.9	15	14	US-10-056-583-25	Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
US-10-056-583-95  
; Sequence 95, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Maisha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; TITLE OF INVENTION: CONDITIONS  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 95  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-95

Query Match 100.0%; Score 69; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e+05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
| | | | | | | | | | | | | | |  
Db 1 EKAKFEAFKAAAAA 15

RESULT 2  
US-10-056-583-96



; Sequence 96, Application US/10056583  
 ; Publication No. US20030064915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presidents and Fellows of Harvard College  
 ; APPLICANT: Strominger, Jack L.  
 ; APPLICANT: Fridkis-Hareli, Masha  
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
 ; FILE REFERENCE: 24655-017  
 ; CURRENT APPLICATION NUMBER: US/10/056,583  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,569  
 ; PRIOR FILING DATE: 2001-01-24  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 96  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: The peptide was designed and synthesized.  
 US-10-056-583-96

Query Match 92.8%; Score 64; DB 14; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 0.00043;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
 |||||:|||||  
 Db 3 EKAKFEAFKAAAAA 17

RESULT 3  
 US-10-056-583-65  
 ; Sequence 65, Application US/10056583  
 ; Publication No. US20030064915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presidents and Fellows of Harvard College  
 ; APPLICANT: Strominger, Jack L.  
 ; APPLICANT: Fridkis-Hareli, Masha  
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
 ; FILE REFERENCE: 24655-017  
 ; CURRENT APPLICATION NUMBER: US/10/056,583  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,569  
 ; PRIOR FILING DATE: 2001-01-24  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 65  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: The peptide was designed and synthesized.  
 US-10-056-583-65

Query Match 91.3%; Score 63; DB 14; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 0.00055;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
 |||||:|||||  
 Db 1 EKAKYEAYKAAAAA 15

RESULT 4  
 US-10-056-583-88  
 ; Sequence 88, Application US/10056583  
 ; Publication No. US20030064915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presidents and Fellows of Harvard College  
 ; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha  
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
 ; FILE REFERENCE: 24655-017  
 ; CURRENT APPLICATION NUMBER: US/10/056,583  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,569  
 ; PRIOR FILING DATE: 2001-01-24  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 88  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: The peptide was designed and synthesized.  
 US-10-056-583-88

Query Match 91.3%; Score 63; DB 14; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 0.00063;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
 |||||:|||||  
 Db 3 EKAKYEAYKAAAAA 17

RESULT 5  
 US-10-056-583-90  
 ; Sequence 90, Application US/10056583  
 ; Publication No. US20030064915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presidents and Fellows of Harvard College  
 ; APPLICANT: Strominger, Jack L.  
 ; APPLICANT: Fridkis-Hareli, Masha  
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
 ; FILE REFERENCE: 24655-017  
 ; CURRENT APPLICATION NUMBER: US/10/056,583  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: 60/263,569  
 ; PRIOR FILING DATE: 2001-01-24  
 ; NUMBER OF SEQ ID NOS: 99  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 90  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: The peptide was designed and synthesized.  
 US-10-056-583-90

Query Match 91.3%; Score 63; DB 14; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 0.00063;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
 |||||:|||||  
 Db 1 EKAKYEAYKAAAAA 15

RESULT 6  
 US-10-056-583-89  
 ; Sequence 89, Application US/10056583  
 ; Publication No. US20030064915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presidents and Fellows of Harvard College  
 ; APPLICANT: Strominger, Jack L.  
 ; APPLICANT: Fridkis-Hareli, Masha  
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
 ; FILE REFERENCE: 24655-017  
 ; CURRENT APPLICATION NUMBER: US/10/056,583



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; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
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Query Match          91.3%; Score 63; DB 14; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.00071;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 EKAKFEAFKAAAAA 15
    |||||:|||||
Db 3 EKAKYEAYKAAAAA 17
```

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RESULT 7
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match          88.4%; Score 61; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0014;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 EKAKFEAFKAAAAA 15
    |||||:|||||
Db 3 EKAKFEAYKAAAAA 17
```

```
RESULT 8
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match          82.6%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0056;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 EKAKFEAFKAAAAA 15
    |||||:|||||
Db 1 EAKYEAYKAAAAA 15
```

```
RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92
```

```
Query Match          82.6%; Score 57; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0056;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 1 EKAKFEAFKAAAAA 15
    |||||:|||||
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 10
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```



; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-91

Query Match 81.2%; Score 56; DB 14; Length 15;  
Best Local Similarity 80.0%; Pred. No. 0.0082;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
|||:|||||  
Db 1 EKPKYAYKAAAAA 15

## RESULT 11

US-10-056-583-57  
; Sequence 57, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-57

Query Match 76.8%; Score 53; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.026;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
|||:|||||  
Db 1 EAKYAYKAAAAA 15

## RESULT 12

US-10-056-583-85  
; Sequence 85, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-85

Query Match 76.8%; Score 53; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.026;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
|||:|||||  
Db 1 EKPKYAYKAAAAA 15

## RESULT 13

US-10-056-583-66  
; Sequence 66, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-66

Query Match 75.4%; Score 52; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.038;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
|||:|||||  
Db 1 EAKYAYKAAAAA 15

## RESULT 14

US-10-056-583-51  
; Sequence 51, Application US/10056583  
; Publication No. US20030064915A1  
; GENERAL INFORMATION:  
; APPLICANT: Presidents and Fellows of Harvard College  
; APPLICANT: Strominger, Jack L.  
; APPLICANT: Fridkis-Hareli, Masha  
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING  
; FILE REFERENCE: 24655-017  
; CURRENT APPLICATION NUMBER: US/10/056,583  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/263,569  
; PRIOR FILING DATE: 2001-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The peptide was designed and synthesized.  
US-10-056-583-51

Query Match 73.9%; Score 51; DB 14; Length 15;  
Best Local Similarity 73.3%; Pred. No. 0.056;  
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15  
|||:|||||  
Db 1 EAKYAYKAAAAA 15



```

RESULT 15
US-10-056-583-53
; Sequence 53, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53

```

```

Query Match      73.9%; Score 51; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.056;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 EKAKFEAFKAAAAA 15
      ||| : |||||
Db      1 EKAAVAAYKAAAAA 15

```

```

Search completed: March 31, 2005, 02:48:49
Job time : 67.5323 secs

```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds  
(without alignments)  
80.614 Million cell updates/sec

Title: US-10-056-583A-95  
Perfect score: 69  
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47.5	68.8	189	2 S77930	exoskeletal protei
2	47.5	68.8	189	2 S77935	exoskeletal protei
3	42	60.9	179	2 F97683	50S ribosomal prot
4	42	60.9	179	2 A2908	50S ribosomal prot
5	41	59.4	346	2 C82156	conserved hypotet
6	41	59.4	828	2 F96535	hypothetical prote
7	40	58.0	478	2 S04675	H+-transporting tw
8	40	58.0	698	2 T32594	hypothetical prote
9	39	56.5	73	2 S40015	phd protein - phag
10	39	56.5	113	2 T30041	hypothetical prote
11	39	56.5	144	2 D83152	hypothetical prote
12	39	56.5	198	2 A12622	conserved hypotet
13	39	56.5	217	2 A97405	hypothetical prote
14	39	56.5	250	2 T51971	proteasome endopep
15	39	56.5	389	2 G87332	hypothetical prote
16	39	56.5	421	2 J00057	colA protein - Esc
17	39	56.5	2957	2 T33152	hypothetical prote
18	38	55.1	151	1 G6ICEH	globin CRT-VIII -
19	38	55.1	246	2 B72728	probable ribosomal
20	38	55.1	320	2 S76422	hypothetical prote
21	38	55.1	436	2 T31902	hypothetical prote
22	38	55.1	510	2 S35028	protein P52 precu
23	38	55.1	525	1 Q0BE6	BFLF1 protein - hu
24	37	53.6	231	2 T02585	hypothetical prote
25	37	53.6	254	2 H86355	probable 14-3-3 pr
26	37	53.6	270	2 G82108	conserved hypotet
27	37	53.6	359	2 H95865	probable fructose-
28	37	53.6	476	2 C72016	glycogen synthase
29	37	53.6	476	2 B86609	glycogen synthase

30	37	53.6	575	2 AC0364	phosphoenolpyruvat
31	37	53.6	795	2 F75154	cell division cont
32	37	53.6	829	2 E64114	translation initia
33	37	53.6	840	2 D75046	transitional endop
34	37	53.6	1430	2 T34516	hypothetical prote
35	37	53.6	1465	2 S43529	165K protein, skel
36	36	52.2	162	2 H70927	probable rpsp prot
37	36	52.2	165	2 B87702	ribosomal protein
38	36	52.2	206	2 S43445	translation elonga
39	36	52.2	251	2 C70521	1-acylglycerol-3-p
40	36	52.2	273	2 T51010	hypothetical prote
41	36	52.2	287	2 T51011	hypothetical prote
42	36	52.2	305	1 R5DOP0	ribosomal protein
43	36	52.2	306	2 C70410	hypothetical prote
44	36	52.2	320	2 B86255	hypothetical prote
45	36	52.2	321	2 A44230	phthalate dioxygen

ALIGNMENTS

RESULT 1

S77930  
exoskeletal protein HACP202A - American lobster (fragment)  
C:Species: Homarus americanus (American lobster)  
C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77930  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus  
A:Reference number: S77925  
A:Accession: S77930  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M496

Query Match 68.8%; Score 47.5; DB 2; Length 189;  
Best Local Similarity 75.0%; Pred. No. 1.3;  
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EKAKFEAFKAAAAA 15  
|||: |||||  
Db 11 EKARFFQAFKAAAAA 26

RESULT 2

S77935  
exoskeletal protein HACP202B - American lobster (fragment)  
C:Species: Homarus americanus (American lobster)  
C:Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S77935  
R:Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.  
submitted to the Protein Sequence Database, June 1997  
A:Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus  
A:Reference number: S77925  
A:Accession: S77935  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-189 <NOU>  
A:Cross-references: UNIPROT:Q7M495

Query Match 68.8%; Score 47.5; DB 2; Length 189;  
Best Local Similarity 75.0%; Pred. No. 1.3;  
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EKAKFEAFKAAAAA 15  
|||: |||||  
Db 11 EKARFFQAFKAAAAA 26

RESULT 3

F97683



50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
 C:Species: Agrobacterium tumefaciens  
 C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
 C:Accession: F97683  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: F97683  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-179 <KUR>  
 A:Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK8423.1; PID:gl5157917; GSPDB:G04675  
 C:Genetics:  
 A:Gene: AGR\_C\_4900  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 60.9%; Score 42; DB 2; Length 179;  
 Best Local Similarity 66.7%; Pred. No. 9.5;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
 |||||  
 Db 137 EKARLEAEKVAQA 151

RESULT 4  
 A:Reference number: AB2577; MUID:21608550; PMID:11743193  
 A:Accession: AF2908  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-179 <KUR>  
 A:Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:gl7741210; GSPDB:G04675  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: rplS  
 A:Map position: circular chromosome  
 C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 60.9%; Score 42; DB 2; Length 179;  
 Best Local Similarity 66.7%; Pred. No. 9.5;  
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
 |||||  
 Db 137 EKARLEAEKVAQA 151

RESULT 5  
 conserved hypothetical protein VCI1791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
 C:Species: Vibrio cholerae  
 C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: C82156  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: C82156  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-346 <HEI>  
 A:Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:99656310; PIDN:AAF9494  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VCI1791  
 A:Map position: 1

Query Match 59.4%; Score 41; DB 2; Length 346;  
 Best Local Similarity 90.0%; Pred. No. 25;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 EAFKAAAAAA 15  
 |||||  
 Db 307 EAFKSAAAAA 316

RESULT 6  
 A:Reference number: F96535  
 A:Accession: F96535  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-828 <STO>  
 A:Cross-references: UNIPROT:Q9C6C7; GB:AE005173; NID:gl0092168; PIDN:AAG12588.1; GSPDB:G04675  
 A:Experimental source: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: F96535  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Mafti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: F96535  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-828 <STO>  
 A:Cross-references: UNIPROT:Q9C6C7; GB:AE005173; NID:gl0092168; PIDN:AAG12588.1; GSPDB:G04675  
 C:Genetics:  
 A:Gene: F10F5.13  
 A:Map position: 1

Query Match 59.4%; Score 41; DB 2; Length 828;  
 Best Local Similarity 69.2%; Pred. No. 56;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAA 13  
 |||||  
 Db 158 EKAAVEAFEAASA 170

RESULT 7  
 A:Reference number: S04675  
 A:Accession: S04675  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-478 <TYB>  
 A:Cross-references: UNIPROT:P05440  
 A:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase alpha subunit; ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding; F155-162/Region: nucleotide-binding motif A (P-loop)

H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Rhodospseudomonas blastica  
 C:Species: Rhodospseudomonas blastica  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C:Accession: S04675  
 R:Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.  
 J. Mol. Biol. 179, 185-214, 1984  
 A>Title: Rhodospseudomonas blastica atp operon. Nucleotide sequence and transcription.  
 A:Reference number: S04666; MUID:85058188; PMID:6209404  
 A:Accession: S04675  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-478 <TYB>  
 A:Cross-references: UNIPROT:P05440  
 A:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase alpha subunit; ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding; F155-162/Region: nucleotide-binding motif A (P-loop)



F1181-357/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 58.0%; Score 40; DB 2; Length 478;  
Best Local Similarity 66.7%; Pred. No. 49;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
: : : : :  
Db 464 EAKAKAAKAAAAA 478

RESULT 8  
T32594  
hypothetical protein C02B10.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T32594  
R:Nelson, J.; White, S.; Hawkins, J.; Wohldmann, P.  
submitted to the EMBL Data Library, December 1997  
A:Description: The sequence of C. elegans cosmid C02B10.  
A:Reference number: Z21196  
A:Accession: T32594  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-598 <NEL>  
A:Cross-references: UNIPROT:O44447; EMBL:AF038605; PIDN:AAB92020.1; GSPDB:GN000022; CESP:  
A:Experimental source: strain Bristol N2; clone C02B10  
C:Genetics:  
A:Gene: CESP:C02B10.5  
A:Map position: 4  
A:Introns: 61/3; 102/2; 188/3; 349/2; 641/1

Query Match 58.0%; Score 40; DB 2; Length 698;  
Best Local Similarity 66.7%; Pred. No. 70;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
: : : : :  
Db 508 QMAHFNQAQAAAAA 522

RESULT 9  
S40015  
phd protein - phase P1  
C:Species: phase P1  
C>Date: 25-Dec-1994 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S40015; S38553  
R:Lehnher, H.; Meguin, E.; Jafri, S.; Yarmolinsky, M.B.  
J. Mol. Biol. 233, 414-428, 1993  
A:Title: Plasmid addition genes of bacteriophage P1: doc, which causes cell death on cu  
A:Reference number: S40015; MUID:94016561; PMID:8411153  
A:Accession: S40015  
A:Molecule type: DNA  
A:Residues: 1-73 <LEH>  
A:Cross-references: UNIPROT:Q06253; GB:M95666; NID:9463276; PIDN:AAA16932.1; PID:9215645  
R:Schmidt, C.; Lehnher, H.; Guidolin, A.; Arber, W.  
submitted to the EMBL Data Library, November 1992  
A:Description: Additional late promoter sequences of bacteriophage P1.  
A:Reference number: S38553  
A:Accession: S38553  
A:Molecule type: DNA  
A:Residues: 1-73 <SCH>  
A:Cross-references: EMBL:M95666; NID:9463276; PIDN:AAA16932.1; PID:9215645

Query Match 56.5%; Score 39; DB 2; Length 73;  
Best Local Similarity 64.3%; Pred. No. 13;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KAKFEAFKAAAAA 15  
: : : : :  
Db 41 KATFEAYKKAALDA 54

RESULT 10  
T30041

hypothetical protein F20A1.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30041  
R:Gattung, S.; Wu, X.  
submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid F20A1.  
A:Reference number: Z20726  
A:Accession: T30041  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-113 <GAT>  
A:Cross-references: UNIPROT:Q19615; EMBL:U53150; PIDN:AAA96131.1; GSPDB:GN000023; CESP:F2  
A:Experimental source: strain Bristol N2; clone F20A1  
C:Genetics:  
A:Gene: CESP:F20A1.1  
A:Map position: 5  
A:Introns: 22/1  
C:Superfamily: Caenorhabditis elegans hypothetical protein F57E7.1

Query Match 56.5%; Score 39; DB 2; Length 113;  
Best Local Similarity 68.8%; Pred. No. 19;  
Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 EKAK--FEAFKAAAAA 14  
: : : : :  
Db 95 EKAKEHFQAKKEAAAA 110

RESULT 11  
D83152

hypothetical protein PA3956 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: D83152  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: D83152  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <STO>  
A:Cross-references: UNIPROT:Q9HX60; GB:AE004813; GB:AE004091; NID:99950134; PIDN:AG0734  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: PA3956

Query Match 56.5%; Score 39; DB 2; Length 144;  
Best Local Similarity 64.3%; Pred. No. 24;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAKFEAFKAAAAA 15  
: : : : :  
Db 82 KAQVDAFHAAALAA 95

RESULT 12  
AI2622

conserved hypothetical protein Atu0377 [imported] - Agrobacterium tumefaciens (strain C5  
C:Species: Agrobacterium tumefaciens  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AI2622  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.



A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: A12622

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-198 <KUR>

A;Cross-references: UNIPROT:Q8UIC0; GB:AE008688; PIDN:AAL41399.1; PID:g17738717; GSPDB:G

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu0377

A;Map position: circular chromosome

Query Match 56.5%; Score 39; DB 2; Length 198;

Best Local Similarity 80.0%; Pred. No. 32;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 KAKFEAFKAA 11

Db 95 KAKMEAFRAA 104

#### RESULT 13

A97405

Hypothetical protein AGR\_C\_660 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004

C;Accession: A97405

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: A97405

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-217 <KUR>

A;Cross-references: UNIPROT:Q8UIC0; GB:AE007869; PIDN:AAK86194.1; PID:g15155291; GSPDB:G

C;Genetics:

A;Gene: AGR\_C\_660

A;Map position: circular chromosome

Query Match 56.5%; Score 39; DB 2; Length 217;

Best Local Similarity 80.0%; Pred. No. 35;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 2 KAKFEAFKAA 11

Db 114 KAKMEAFRAA 123

#### RESULT 14

T51971

proteasome endopeptidase complex (EC 3.4.25.1) chain PAD2 [imported] - Arabidopsis thali

N;Alternate names: 20S proteasome chain PAD2

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004

C;Accession: T51971

R;Fu, H.; Doelling, J.H.; Arendt, C.S.; Hochstrasser, M.; Vierstra, R.D.

Genetics 149, 677-692, 1998

A;Title: Molecular organization of the 20S proteasome gene family from Arabidopsis thali

A;Reference number: Z5275; MUID:961183; PMID:961183

A;Accession: T51971

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-250 <FUH>

A;Cross-references: UNIPROT:Q24616; EMBL:AF043523; PIDN:AAC32059.1

A;Experimental source: strain Columbia; seedling hypocotyls

C;Genetics:

A;Note: PAD2

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase; proteinase

Query Match 56.5%; Score 39; DB 2; Length 250;

Best Local Similarity 76.9%; Pred. No. 40;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKFEAFKAAAAA 15

Db 230 AKTEAKAAAAAA 242

#### RESULT 15

G87332

hypothetical protein CC0674 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C;Accession: G87332

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: G87332

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <STO>

A;Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:G

C;Genetics:

A;Gene: CC0674

Query Match 56.5%; Score 39; DB 2; Length 389;

Best Local Similarity 64.3%; Pred. No. 60;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 KAKFEAFKAAAAA 15

Db 66 KTSVETFKAAAAA 79

Search completed: March 31, 2005, 02:42:30

Job time : 18.9032 secs



Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	47.5	68.8	189	2	Q7M495	Q7m495 homarus ame
2	47.5	68.8	189	2	Q7M496	Q7m496 homarus ame
3	44	63.8	707	2	Q64CP3	Q64cp3 uncultured
4	43	62.3	99	2	Q6ERT5	Q6ert5 oryza sativ
5	43	62.3	299	1	RL22_DROME	P50887 drosophila
6	43	62.3	312	2	Q9UAN1	Q9uan1 drosophila
7	42	60.9	177	1	RL19_RHIME	Q92139 rhizobium m
8	42	60.9	179	1	RL19_AGRT5	Q8ubz5 agrobacteri
9	42	60.9	181	1	RL19_RHILO	P58168 rhizobium l
10	42	60.9	274	2	Q6UK87	Q6uk87 burkholderi
11	42	60.9	385	2	Q6W1S9	Q6wis9 rhizobium s
12	42	60.9	396	2	Q6D7F3	Q6d7f3 erwinia car
13	42	60.9	508	2	Q6OUT5	Q6out5 corynebacte
14	41	59.4	344	2	Q7OLQ4	Q7olq4 anopheles g
15	41	59.4	346	2	Q9XR55	Q9xr55 vibrio chol
16	41	59.4	734	2	Q9RC4	Q9rc4 rhizobium l
17	41	59.4	828	2	Q9C6C7	Q9c6c7 arabidopsis
18	40	58.0	366	2	Q6FT73	Q6ft73 candida gla
19	40	58.0	369	2	Q6S0Y0	Q6s0y0 oryza sativ
20	40	58.0	478	1	Q6YWS1	Q6yws1 oryza sativ
21	40	58.0	415	1	ATPB_RHOBL	P05440 rhodopseudo
22	40	58.0	614	2	Q64JV2	Q64jv2 plasmodium
23	40	58.0	698	2	Q44447	Q44447 caenorhabdi
24	40	58.0	760	2	Q8GA14	Q8ga14 dictyosteli
25	40	58.0	3247	2	Q65553	Q65553 bovine herp
26	40	58.0	3247	2	Q77CD4	Q77cd4 bovine herp
27	39	56.5	41	2	Q84W05	Q84w05 arabidopsis
28	39	56.5	73	1	PHD_BPPI	Q06253 bacterioph
29	39	56.5	73	2	Q79A04	Q79a04 escherichia
30	39	56.5	113	2	Q19615	Q19615 caenorhabdi
31	39	56.5	144	2	Q9HX60	Q9hx60 pseudomonas

[illegible]



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Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 EKAK-FAAFKAAAAA 15
   |||: |||: |||: |||:
Db 11 EKARFFQAFKAAEA 26

RESULT 3
Q64CP3
ID Q64CP3 PRELIMINARY; PRT; 707 AA.
AC Q64CP3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ1D1.21;
OS uncultured archaeon GZfos1D1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY14833; AAU82834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match 63.8%; Score 44; DB 2; Length 707;
Best Local Similarity 73.3%; Pred. No. 79;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
   |||: |||: |||: |||:
Db 645 EKLKSEAEAAAAA 659

RESULT 4
Q6ERT5
ID Q6ERT5 PRELIMINARY; PRT; 99 AA.
AC Q6ERT5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dynein light chain type 1-like.
GN Name=P0693E08.27;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasakii T., Matsumoto T., Katayose Y.;
RL EMBL; AF005428; BAD28635.1; -.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007017; P:microtubule-based process; IEA.
DR InterPro; IPR001372; Dynein_light1.
DR Pfam; PF01221; Dynein_light1.
DR ProDom; PD005145; Dynein_light1.
SQ SEQUENCE 99 AA; 10617 MW; 3BD39F5BA41561E6 CRC64;

Query Match 62.3%; Score 43; DB 2; Length 99;

Best Local Similarity 66.7%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
   |||: |||: |||: |||:
Db 81 ERLSFLFKAAAAA 95

RESULT 5
RL22_DROME
ID RL22_DROME STANDARD; PRT; 299 AA.
AC P50887; Q9V3X9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE 60S ribosomal protein L22.
GN Name=Rpl22; ORFNames=CG7434;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Glover C.V.C., Bidwai A.P., Zhao W.F.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
```



RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.K., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Oregon-R;  
RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;  
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,  
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,  
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,  
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,  
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,  
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,  
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,  
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
RA Glover D.M.;  
RT "From sequence to chromosome: the tip of the X chromosome of D.  
RT melanogaster";  
RL Science 287:2220-2222(2000).  
CC -!- SIMILARITY: Belongs to the ribosomal protein L22e family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC  
DR EMBL; U42587; AAB17433.1; -;  
DR EMBL; AB003448; AAF45546.1; -;  
DR EMBL; AL132792; CAB60023.1; -;  
DR InAct; P50887; -;  
DR FlyBase; FBgn0015288; RPL22.  
DR InterPro; IPR002671; Ribosomal\_L22e.  
DR Pfam; PF01776; Ribosomal\_L22e; 1.  
DR ProDom; PD007306; Ribosomal\_L22e; 1.  
KW Ribosomal protein.  
FT DOMAIN 24 31 Poly-Ala.  
FT DOMAIN 46 50 Poly-Ala.  
FT DOMAIN 65 70 Poly-Ala.  
FT DOMAIN 93 98 Poly-Ala.  
FT DOMAIN 103 112 Poly-Ala.  
FT DOMAIN 136 152 Poly-Ala.  
FT DOMAIN 185 188 Poly-Lys.  
FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).  
SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;  
  
Query Match 62.3%; Score 43; DB 1; Length 299;  
Best Local Similarity 73.3%; Pred. No. 52;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 EKAKFEAFKAAAAA 15  
Db 36 EKPKAAEAAPAAAAA 50  
  
RESULT 6  
Q9UAN1 PRELIMINARY; PRT; 312 AA.  
AC Q9UAN1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein L22 (Fragment).  
GN Name=RPL22; Synonyms=rpL22;  
OS Drosophila melanogaster (Fruit fly).  
DR

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;  
RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;  
RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal  
RT proteins, L22 and L23a, with unique histone-like amino-terminal  
RT extensions";  
RL Gene 226:339-345(1999).  
DR EMBL; AF080131; AAD19341.1; -;  
DR FlyBase; FBgn0015288; RPL22.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR InterPro; IPR002671; Ribosomal\_L22e.  
DR Pfam; PF01776; Ribosomal\_L22e; 1.  
KW Ribosomal protein.  
FT NON TER 1  
SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;  
  
Query Match 62.3%; Score 43; DB 2; Length 312;  
Best Local Similarity 73.3%; Pred. No. 55;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 EKAKFEAFKAAAAA 15  
Db 49 EKPKAAEAAPAAAAA 63  
  
RESULT 7  
RL19\_RHIME STANDARD; PRT; 177 AA.  
ID RL19\_RHIME  
AC Q92L39;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE 50S ribosomal protein L19.  
GN Name=rpL19; OrderedLocustNames=R03246; ORFNames=SMC03863;  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
RA Godard T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampsberger U.,  
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont  
RT Sinorhizobium meliloti strain 1021";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit  
CC interface and may play a role in the structure and function of the  
CC aminoacyl-tRNA binding site (By similarity).  
CC -!- SIMILARITY: Belongs to the ribosomal protein L19p family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC  
DR EMBL; AL591793; CAC47825.1; -;  
DR HAMAP; MF\_00402; -; 1.  
DR



Query Match	60.9%;	Score 42;	DB 1;	Length 181;
Best Local Similarity	66.7%;	Pred. No. 49;		



Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
| | | | | | | | | |  
Db 136 EKARIEAEKVAQA 150

## RESULT 10

Q6UK87 PRELIMINARY; PRT; 274 AA.  
AC Q6UK87; (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Gp4.  
GN Name=ORF64;  
OS Burkholderia cepacia phage Bcep43.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
OX NCBI\_TaxID=260373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Summer E.J., Bomer M.L., Bean E.D., Embry A.E., Mebane L.M.,  
RA Tsou L.L.-C., No E.-G., Gonzalez C.F., Young R.F.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY368235; AAR89355.1; --  
SQ SEQUENCE 274 AA; 28795 MW; 14419D38C3112965 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 274;  
Best Local Similarity 71.4%; Pred. No. 71;  
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAKFEAFKAAAAA 15  
| | | | | | | | | |  
Db 116 KAEIEADKAAAAAS 129

## RESULT 11

Q6W1S9 PRELIMINARY; PRT; 386 AA.  
AC Q6W1S9;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Spermidine/putrescine-binding protein.  
GN ORFNames=NGR00516;  
OS Rhizobium sp. (strain NGR234).  
OC Plasmid megaplasmid 2.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Broughton W.J., Perret X., Staehelin C., Schmitz R.A., Raasch C.,  
RA Liesegang H., Gottschalk G., Streit W.R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY316747; AA087289.1; --  
DR HSSP; P31133; 1A99.  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006059; SBP\_bac.1.  
DR InterPro; IPR001188; Sperm/putr-bndng.  
DR Pfam; PF01547; SBP\_bac.1; 1.  
DR PRINTS; PR00909; SPERMNDNDNG.  
DR TIGRPFAMs; TIGR01409; TAT\_signal\_seq; 1.  
KW Plasmid.  
SQ SEQUENCE 386 AA; 42194 MW; 5856D6447B3B42F4 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 386;  
Best Local Similarity 60.0%; Pred. No. 97;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
| | | | | | | | | |  
Db 76 DPATFEAFKAATGVA 90

## RESULT 12

Q6D7F3 PRELIMINARY; PRT; 395 AA.  
AC Q6D7F3;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Tola protein.  
GN Name=tola; OrderedLocusNames=ECAL372;  
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=29471;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=SCRI 1043 / ATCC BAA-672;  
RC PubMed=15263089; DOI=10.1073/pnas.0402424101;  
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,  
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,  
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,  
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,  
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,  
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;  
RT "Genome sequence of the enterobacterial phytopathogen Erwinia  
RT carotovora subsp. atroseptica and characterization of virulence  
RT factors";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).  
DR EMBL; BX950851; CAG74282.1; --  
DR InterPro; IPR010528; Tola.  
DR Pfam; PF06519; Tola; 1.  
KW Complete proteome.  
SQ SEQUENCE 395 AA; 41698 MW; 2DB1DAA64E984199 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 395;  
Best Local Similarity 73.3%; Pred. No. 99;  
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15  
| | | | | | | | | |  
Db 205 ETAKAEAKAAAEAA 219

## RESULT 13

Q6QUT5 PRELIMINARY; PRT; 508 AA.  
AC Q6QUT5;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE PS2.  
OS Corynebacterium glutamicum (Brevibacterium flavum).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=1718;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=22243;  
RC PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;  
RA Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tauch A.,  
RA Puhler A., Kalinowski J.;  
RT "Classification of hyper-variable Corynebacterium glutamicum surface-  
RT layer proteins by sequence analyses and atomic force microscopy.";  
RL J. Biotechnol. 112:177-193(2004).  
DR EMBL; AY525006; AAS20307.1; --  
SQ SEQUENCE 508 AA; 55416 MW; B28137E469228581 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 508;



